

83384

From: Chan, Christina
 Sent: Tuesday, December 31, 2002 1:08 PM
 To: Holleran, Anne; STIC-Biotech/ChemLib
 Subject: RE: RUSH sequence search for 09/806,301

Please rush. Thanks

Chris Chan
 TC 1600 New Hire Training Coordinator and SPE 1644
 308-3973
 CM-1, 9B19

Point of Contact:
 Mona Smith
 Technical Information Specialist
 CM1 6A01
 Tel: 308-3278

-----Original Message-----

From: Holleran, Anne
 Sent: Tuesday, December 31, 2002 1:06 PM
 To: Chan, Christina
 Subject: RUSH sequence search for 09/806,301

Please approve and forward to STIC this RUSH sequence search request. This is an amendment due this biweek. Thanks.

Please search the following:

commercial and interference databases search of SEQ ID NO: 2(aa)

commercial and interference databases **oligomer** search of SEQ ID NO: 2(aa)

Anne Holleran
 AU: 1642
 Tel: 308-8892
 RM: 8e03

mailbox: 8e12

Searcher: H. Smith
 Phone: _____
 Location: _____
 Date Picked Up: 1/2/03
 Date Completed: 1/3/03
 Searcher Prep/Review: 2
 Clerical: _____
 Online time: 7

TYPE OF SEARCH:

NA Sequences: _____
 AA Sequences: 2
 Structures: _____
 Bibliographic: _____
 Litigation: _____
 Full text: _____
 Patent Family: _____
 Other: _____

VENDOR/COST (where applic.)

STN: _____
 DIALOG: _____
 Questel/Orbit: _____
 DRLink: _____
 Lexis/Nexis: _____
 Sequence Sys.: _____
 WWW/Internet: _____
 Other (specify): _____

Point of Contact
Mona Smith
Technical Information Specialist
OMI 6A01
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:53:07 ; Search time 29 Seconds

(without alignments)
639,457 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 450
Sequence: 1 MKLSVCLLVLTALCCYQAN.....LQKRSLAEVLKIKCSV 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249	55.3	90	6	O9GK67 oryctolagus
2	245	54.4	96	6	O8WMS2 oryctolagus
3	231.5	50.2	91	6	O9GK66 oryctolagus
4	226	50.2	90	6	O9GK65 oryctolagus
5	91	20.2	95	4	O8TD33 homo sapien
6	85	18.9	96	11	O8VD96 mesocricetu
7	78.5	17.4	317	11	O8VFE6 mus musculu
8	77.5	17.2	94	11	O05702 rattus ratu
9	70.5	15.7	320	11	O8VFE6 mus musculu
10	69	15.3	167	11	O9QWLS mus musculu
11	69	15.3	1622	10	O48908 arabidopsis
12	69	15.3	1623	10	O48907 arabidopsis
13	69	15.3	1623	10	O64590 arabidopsis
14	68.5	15.2	1623	10	O22449 arabidopsis
15	68	15.1	290	10	O8W3C2 oryza sativ
16	67	14.9	74	10	O8W2V1 oryza sativ

17	66.5	14.8	434	5	O9VZA6 drosophila
18	66.5	14.8	578	5	O9XVG0 caenorhabd
19	66	14.7	102	16	O8U5C3 agrobacteri
20	65.5	14.6	310	5	O97466 trypanosoma
21	65.5	14.6	310	5	O96649 trypanosoma
22	65.5	14.6	415	4	O9Y614 homo sapien
23	65.5	14.6	415	6	O95JK8 macaca fasc
24	65	14.4	470	10	O8S9A4 phaseolus a
25	64	14.2	213	5	O9VBO4 drosophila
26	64	14.2	366	5	O9U0W2 leishmania
27	64	14.2	797	10	O9FW44 arabidopsis
28	63	14.0	115	11	O9DAK3 mus musculu
29	63	14.0	446	4	O96EF4 mus musculu
30	63	14.0	446	4	O9NVH3 homo sapien
31	63	14.0	473	4	O9H384 homo sapien
32	63	14.0	676	4	O9BQ70 homo sapien
33	63	14.0	735	4	O9H7V5 homo sapien
34	63	14.0	756	4	O96ST4 homo sapien
35	63	14.0	796	4	O9P217 homo sapien
36	63	14.0	1354	10	O948F4 oryza sativ
37	63	14.0	1862	10	O94104 oryza sativ
38	63	14.0	2029	5	O9VD07 drosophila
39	62.5	13.9	90	13	O9PWA6 gallus gall
40	62.5	13.9	90	13	O910C9 gallus gall
41	62.5	13.9	371	5	O16474 caenorhabd
42	62.5	13.9	844	3	O96X45 neurospora
43	62.5	13.9	929	16	O98R55 mycoplasma
44	62	13.8	155	5	O9V6U0 drosophila
45	62	13.8	167	4	O9UED4 homo sapien

ALIGNMENTS

RESULT 1					
O9GK67		PRELIMINARY;	PRT;	90 AA.	
AC O9GK67:					
DT 01-MAR-2001 (TREMBLrel. 16, Created)					
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)					
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)					
DE Lipophilin AL.					
OS Oryctolagus cuniculus (Rabbit).					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.					
OX NCBI_TaxID=9986;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC TISSUE=LACRIMAL GLAND;					
RA Zhao C., Nguyen T.X., Lehrer R.I.;					
RT "Rabbit Lipophilins.";					
Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.					
DR EMBL: AF308614; AAC42802.1; -					
DR InterPro: IPR000329; Uterogloblin.					
DR Pfam: PF01099; Uterogloblin; 1.					
DR SMART: SM00096; UMG; 1.					
DR SEQUENCE 90 AA; 9762 MW; 6034F9540C1FF742 CRC64;					
QY	1	MKLSVCLLVLTALCCYQANAERCPALVSELDFFFLSEFLSLAKFPAPPEVAAKL	60		
DB	1	MKLLVPLLVLTALVLCGEADAACPAFLVDSVFLDPKPVYRKLAKYDAPPEVAAKL	60		
QY	61	GVKRCIDMSLQKRSILAELVKIKKCSV	90		
DB	61	QVKECDTDEIKGRVLIANVLTKIVKCAI	90		
RESULT 2					
O8WMS2					

ID 08WMS2: PRELIMINARY: PRT: 96 AA.
 AC 08WMS2:
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Lipophilin AL2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LACRIMAL GLAND;
 RA Lind-Ayres M.R., Crow J.M., Steelman C.A., Nelson J.D.,
 RA Remington S.G.;
 RT "Lipophilin AL2 of the male rabbit lacrimal gland";
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY063770; AAI40859.1;
 DR InterPro: IPR000329; Uteroglobin.
 DR Pfam: PF01099; Uteroglobin; 1.
 SQ SEQUENCE 96 AA: 10510 MW: 48EC2972DDEA78C4 CRC64;

Query Match 54.4%; Score 245; DB 6; Length 96;
 Best Local Similarity 52.8%; Pred. No. 1,le-21;
 Matches 47; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLPKLSLAKFDAPPEAVAAKL 60
 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLPKLSLAKFDAPPEAVAAKL 60
 DB 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLPKLSLAKFDAPPEAVAAKL 60
 OY 61 GVKRCTDOMSLQKRSLLAEVLVKILKCS 89
 61 GVKRCTDOMSLQKRSLLAEVLVKILKCS 89
 DB 61 NVKRCVNEISLGRKLLIERILGEVLTECS 89

RESULT 3
 O9GK66 PRELIMINARY: PRT: 91 AA.
 AC 09GK66:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Lipophilin AS.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SUBMAXILLARY;
 RA Zhao C., Nguyen T.X., Lehrer R.I.;
 RT "Rabbit Lipophilins";
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF308615; AAG42803.1;
 DR InterPro: IPR000329; Uteroglobin.
 DR Pfam: PF01099; Uteroglobin; 1.
 DR PRINTS: PRO0486; UTEROglobin.
 DR SMART: SMO0096; UTG: 1.
 SQ SEQUENCE 91 AA: 9723 MW: 579DCD0B813554C4 CRC64;

Query Match 51.4%; Score 231.5; DB 6; Length 91;
 Best Local Similarity 51.6%; Pred. No. 4,4e-20;
 Matches 47; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLPKLSLAKFDAPPEAVAAKL 60
 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLPKLSLAKFDAPPEAVAAKL 60
 DB 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLPKLSLAKFDAPPEAVAAKL 60
 OY 61 GVKRCTDOMSLQKRSLLAEVLVKI-LKCSV 90
 61 GVKRCTDOMSLQKRSLLAEVLVKI-LKCSV 90
 DB 61 GVKRCTDOMSLQKRSLLAEVLVKI-LKCSV 90

RESULT 4
 O9GK65 PRELIMINARY: PRT: 90 AA.
 AC 09GK65:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Lipophilin BL.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LACRIMAL GLAND;
 RA Zhao C., Nguyen T.X., Lehrer R.I.;
 RT "Rabbit Lipophilins";
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF308616; AAG42804.1;
 DR InterPro: IPR000329; Uteroglobin.
 DR Pfam: PF01099; Uteroglobin; 1.
 DR PRINTS: PRO0486; UTEROglobin.
 SQ SEQUENCE 90 AA: 9943 MW: 410900DF7F3EB1BC CRC64;

Query Match 50.2%; Score 226; DB 6; Length 90;
 Best Local Similarity 51.1%; Pred. No. 2e-19;
 Matches 46; Conservative 17; Mismatches 27; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLPKLSLAKFDAPPEAVAAKL 60
 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLPKLSLAKFDAPPEAVAAKL 60
 DB 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLPKLSLAKFDAPPEAVAAKL 60
 OY 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90
 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90
 DB 61 TVKCTDGMPEKRNILAGALGEVLIQCPV 90

RESULT 5
 O8TD33 PRELIMINARY: PRT: 95 AA.
 AC 08TD33:
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative ligand binding protein RYD5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bingle C.D.;
 RT "Human RYD5, a new secretoglobulin";
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY026938; AAK08972.1;
 SQ SEQUENCE 95 AA: 10457 MW: F629AF06C96D2392 CRC64;

Query Match 20.2%; Score 91; DB 4; Length 95;
 Best Local Similarity 29.5%; Pred. No. 0.0027;
 Matches 28; Conservative 16; Mismatches 35; Indels 16; Gaps 2;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFIS-----EPLFKLSLAKFD 50
 1 MKGSRALLLVLTALCCYQNAEFCPALVSELDFFIS-----EPLFKLSLAKFD 50
 DB 1 MKGSRALLLVLTALCCYQNAEFCPALVSELDFFIS-----EPLFKLSLAKFD 50
 OY 51 APPEAVAAKLGVKRCTDOMSLQKRSLLAEVLVKIL 85
 51 APPEAVAAKLGVKRCTDOMSLQKRSLLAEVLVKIL 85
 DB 55 VNEDAKAAATELKSQRDGLQPMKAEVLKLVOL 89

RESULT 6
 O8VD96 PRELIMINARY: PRT: 96 AA.
 ID 08VD96

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AC 08VD96;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE CC10 protein precursor.
GN CC10.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Gullerier-Sagal R., Nieto A.;
RT "Cloning and sequencing of a cDNA encoding hamster uteroglobin/clara
cell 10 kDa protein."
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; L37041; AAL31349.1;
DR InterPro; IPR003628; Uteroglobin_sub.
DR InterPro; IPR000329; Uteroglobin.
DR Pfam; PF01099; Uteroglobin; 1.
DR ProDom; PD012475; Uteroglobin_sub; 1.
DR SMART; SM00096; UTE; 1.
DR PROSITE; PS00404; UTEROGLOBIN_2; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 96 AA; 10509 MW; 5EB9CBDD46143389 CRC64;

Query Match
Best Local Similarity 24.4%; Pred. No. 0.014;
Matches 21; Conservative 27; Mismatches 36; Indels 2; Gaps 2;

QY 1 MKLSVCLLVTLALCCQANAEPCPALVSELDFFFT-SEPLFKLSLAKDPAPPAVAK 59
DB 1 MKLAITAAVVALVYCSCSSASSDTCGPF-QLYELFLWGSSESYALAKFTYNPSSLDQDSG 59
QY 60 LGVRCRTDQMSLQKRSLLAEVLVKIL 85
DB 60 TOLKLVDTLPQKTRNMIMKLSFTIL 85

RESULT 7
Q8VFH6 PRELIMINARY; PRT; 317 AA.
ID 08VFH6
AC 08VFH6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Olfactory receptor MOR114-8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RT Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073550; AAL61213.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW Receptor.
SQ SEQUENCE 317 AA; 35896 MW; 6C550A33DD277D24 CRC64;

Query Match 17.4%; Score 78.5; DB 11; Length 317;

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Best Local Similarity 25.3%; Pred. No. 0.28;
Matches 25; Conservative 13; Mismatches 22; Indels 39; Gaps 5;

QY 1 MKLSVCLLVTLALCCQY-----NAECPALVSELDFFFT-SEPLFKSL 46
DB 133 MSSKVC---QTLVLCWSACLLIILPPLTFLNLFCD---SNVIDYFCDASPLIKIS 185
QY 47 AKDPAPPAVAARKGVRCRTDQMSLQKRSLLAEVLVKIL 95
DB 186 -----CSDTWLEQLVAVCAVLTFL 306

RESULT 8
Q05702 PRELIMINARY; PRT; 94 AA.
ID 005702
AC 005702;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE Potential ligand-binding protein.
GN RVD5.
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISCHER; TISSUE=OLFACTORY EPITHELIUM;
RX MEDLINE=92007724; Pubmed=1915264;
RA Dear T.N., Boehm T., Keverne E.B., Rabbits T.H.;
RT "Novel genes for potential ligand-binding proteins in subregions of
the olfactory mucosa."
RT EMBL; J10-2813-2819(1991).
DR EMBL; X60661; CAA43068.1;
DR InterPro; IPR000329; Uteroglobin.
DR SMART; SM00096; UTE; 1.
SQ SEQUENCE 94 AA; 10401 MW; 25A4BBB4977E247 CRC64;

Query Match 17.2%; Score 77.5; DB 11; Length 94;
Best Local Similarity 28.4%; Pred. No. 0.11;
Matches 25; Conservative 15; Mismatches 45; Indels 3; Gaps 2;

QY 1 MKLSVCLLVTLALC-CYQANAEPCPALVSELDFFFTSEPLFKLSLAKDPAPPAVA 57
DB 1 MKSSALIVALTVCICGLTRAEDDNEFFMEFLDTLVGPEELVSPKLYNNDMAKA 60
QY 58 AKLGKRCRTDQMSLQKRSLLAEVLVKIL 85
DB 61 ALTELKSCIDELQPVHKEQLVILVYL 88

RESULT 9
Q8VF26 PRELIMINARY; PRT; 320 AA.
ID 08VF26
AC 08VF26;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Olfactory receptor MOR114-11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RT Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073715; AAL61378.1;

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DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1.1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_FL1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECIP_FL2; 1.
 KW Receptor.
 SQ SEQUENCE 320 AA; 36272 MW; 6C8D7F1078AB6684 CRC64;

Query Match 15.7%; Score 70.5; DB 11; Length 320;
 Best Local Similarity 25.3%; Pred. No. 2.5;
 Matches 25; Conservative 12; Mismatches 23; Indels 39; Gaps 5;

OY 1 MKLSVCLLVTLALCCYQA-----NAECPALVSELDFFFI-SEPLFKLSL 46
 DB 134 MNKVCALIV---LCCWTSGLVIIIPLMILQLFCD---SDTIHFCDASPLKIS- 186
 OY 47 AKFDAPPEVAALKGKRCCTDOMSLDKRSLIAEVLVKIL 85
 DB 187 -----CSDTWLEQIVYVCAVLTFII 207

RESULT 10

OQ9WL5 PRELIMINARY; PRT; 167 AA.

AC OQ9WL5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Murine CMAP (CYSTATIN F) (LEUKOCYSTATIN).
 GN MURINE CMAP OR CS77.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morita M., Aizawa H., Yoshituchi N.;
 RT "A novel cystatin-like metastasis associated gene.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glass C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boicelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustlich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli V., Mombereits P.,
 RA Nardone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmink L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AB015224; BAA34940.1; -;
 DR EMBL: AK004420; BAB32398.1; -;
 DR HSSP: P01034; 1696.
 DR MGP: MGI:1298217; Cst7.
 DR InterPro: IPR000010; Cystatin.
 DR Pfam: PF00031; cystatin; 1.
 DR SMART: SM00043; CY; 1.
 SQ SEQUENCE 167 AA; 18847 MW; 61F776D8445095FE CRC64;

Query Match 15.3%; Score 69; DB 11; Length 167;

Best Local Similarity 27.0%; Pred. No. 2;
 Matches 24; Conservative 22; Mismatches 25; Indels 18; Gaps 5;

OY 8 LVTLALCCYQANA-----ERCPA-LVSELDFFFISEPLFKLSLAKDAPPEVAAL 60
 DB 26 LALIALCCITSDPTGARPDPFCSDLISSV-----KPGPKTI-ETNNGVLAARH 77
 OY 61 GVKR---CTDOMSLDKRSLIAEVLVKIL 86
 DB 78 SVEKFNCTNDITFLFKESHVKALVQVK 106

RESULT 11

O48908 PRELIMINARY; PRT; 1622 AA.

AC O48908;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE MgATP-energized glutathione S-conjugate pump (EC 3.6.1.3).
 GN MRP2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lu Y.-P., Li Z.-S., Drozdowicz Y.M., Hortensteiner S., Martlino E.,
 RA Rea P.A.;

RT "AtMRP2, an Arabidopsis ATP-binding cassette transporter able to
 RT transport glutathione S-conjugates and chlorophyll catabolites:
 RT functional comparisons with AtMRP1.";
 RL Plant Cell 10:1-18(1998).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AF020289; AAC04246.1; -;
 DR HSSP: P13569; INBD.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001140; ABCtransporter.
 DR InterPro: IPR003439; ABC_transporter.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR Pfam: PF00005; ABC_tran; 2.
 DR PRODOM: PD000006; ABC_transporter; 2.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 2.
 KW ATP-binding; Hydrolase; Transport.

SQ SEQUENCE 1622 AA; 182043 MW; 41AA158D694EA42A CRC64;

Query Match 15.3%; Score 69; DB 10; Length 1622;
 Best Local Similarity 36.5%; Pred. No. 19;
 Matches 27; Conservative 9; Mismatches 22; Indels 16; Gaps 5;

OY 3 LSVCLLVTLALCCYQANAECPALVSELDFFFI-----ISEPLFKL-----SLAKPDA 51
 DB 47 LVLCRLRIWLAQDKVFE-RFC--LRSRLYNIFLALLAAYATAEPFLRMIGISVLDPDG 103
 OY 52 P---PEAVNAKGVK 63
 DB 104 PGLPPEFAFGLVK 117

RESULT 12

O48907 PRELIMINARY; PRT; 1623 AA.

AC O48907;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE MgATP-energized glutathione S-conjugate pump (EC 3.6.1.3).
 GN MRP2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lu Y.-P., Li Z.-S., Drodowicz Y.M., Hortensteiner S., Martinoia E.,
 Rea P.A.;
 RT "AtMRP2, an Arabidopsis ATP-binding cassette transporter able to
 transport glutathione S-conjugates and chlorophyll catabolites;
 RT functional comparisons with AtMRP1.";
 RL Plant Cell 10:1-18(1998).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AF020288; AAC04245.1; -
 DR HSSP: P13569; INBD.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001140; ABCtransportrTM.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR Pfam: PF00005; ABC_tran; 2.
 DR ProDom: PD000006; ABC_transportr; 2.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 2.
 DR ATP-binding; Hydrolase; Transporter
 KW SEQUENCE 1623 AA; 182073 MW; 963087B048999970 CRC64;
 SO

Query Match 15.3%; Score 69; DB 10; Length 1623;
 Best Local Similarity 36.5%; Pred. No. 19;
 Matches 27; Conservative 9; Mismatches 22; Indels 16; Gaps 5;

OY 3 LSVCLLVLTALCCYQANMEFCALVSELDFFF-----ISEPLFKL----SLAKFDA 51
 DB 47 LVLCLEIRIMWLAKDHRVE--RFC--LRSLRYNYFLALLAAVATAEPLFRIMGISVLDFO 103
 OY 52 P--PEAVAARKIGVK 63
 DB 104 PGLPPEAFGLGK 117

RESULT 13

064590

ID 064590 PRELIMINARY; PRT; 1623 AA.

AC 064590;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE ABC transporter (AtMRP2).
 GN AT2G34660.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldhahn T.V.,
 Buell C.R., Ketchum K.A., Lee J.J., Konning C.M., Koo H., Motil K.S.,
 Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
 Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 Rasmussen S., Preuss D., Niernman W.C., White O., Eissen J.A.,
 Salberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Lin X.;
 RT Submitted (Mar-2000) to the EMBL/genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AC003096; AAC16268.1; -
 DR HSSP: P13569; INBD.

DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001140; ABCtransportrTM.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR Pfam: PF00005; ABC_tran; 2.
 DR ProDom: PD000006; ABC_transportr; 2.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 2.
 DR ATP-binding; Transporter
 KW SEQUENCE 1623 AA; 182129 MW; F074F0F6ED7A1D47 CRC64;
 SO

Query Match 15.3%; Score 69; DB 10; Length 1623;
 Best Local Similarity 36.5%; Pred. No. 19;
 Matches 27; Conservative 9; Mismatches 22; Indels 16; Gaps 5;

OY 3 LSVCLLVLTALCCYQANMEFCALVSELDFFF-----ISEPLFKL----SLAKFDA 51
 DB 47 LVLCLEIRIMWLAKDHRVE--RFC--LRSLRYNYFLALLAAVATAEPLFRIMGISVLDFO 103
 OY 52 P--PEAVAARKIGVK 63
 DB 104 PGLPPEAFGLGK 117

RESULT 14

022449

ID 022449 PRELIMINARY; PRT; 1623 AA.

AC 022449;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Multidrug resistance-associated protein 2.
 GN ATMRP2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LANDSBERG ERECTA;
 RA MEDLINE-98189246; PubMed-9528668;
 RA Martin E., Leonhardt N., Vavasseur A., Forestier C.;
 RT "Cloning of AtMRP2, an Arabidopsis thaliana cDNA encoding a homologue
 of the mammalian multidrug resistance-associated protein.";
 RL Biochim. Biophys. Acta 1369:7-13(1998).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AF014960; AAC49988.1; -
 DR HSSP: P13569; INBD.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001140; ABCtransportrTM.
 DR InterPro: IPR003439; ABC_transportr.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR Pfam: PF00005; ABC_tran; 2.
 DR ProDom: PD000006; ABC_transportr; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 2.
 DR ATP-binding; Transporter.
 KW SEQUENCE 1623 AA; 181968 MW; 1D17ACE1D0578D33 CRC64;
 SO

Query Match 15.2%; Score 68.5; DB 10; Length 1623;
 Best Local Similarity 35.5%; Pred. No. 22;
 Matches 27; Conservative 6; Mismatches 20; Indels 23; Gaps 5;

OY 9 LVTLALCCYQ-----ANAEFCALVSELDFFF-----ISEPLFKL----SLAKF 49
 DB 44 LVLCLEIRIMWLAKDHRVE--RFC--LRSLRYNYFLALLAAVATAEPLFRIMGISVLDFO 101
 OY 50 DAP--PEAVAARKIGVK 63
 DB 102 DGPLPPEAFGLGK 117

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RESULT 15
ID 08W3C2 PRELIMINARY; PRT: 290 AA.
AC 08W3C2:
DT 01-MAR-2002 (TRENBLREL. 20; Created)
DT 01-MAR-2002 (TRENBLREL. 20; Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21; Last annotation update)
DE Putative polyprotein (Hypothetical 33.4 kDa protein).
GN OSJNB0046102.13 OR OJ136E01.1.
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA Saski C., Henry D., Oates R., Simmons J.;
RT "Rice Genomic Sequence.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPONBARE;
RA McCombie W.R., de la Bastide M., Spiegel L., Preston R., Kirchoff K.,
RA Kuit R., Nascimento L., Zuberer T., Balija V., Bell M., Baker J.,
RA Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,
RA O'Shaughnessy A., Palmer L., Dedha N.;
RT "Genomic sequence for Oryza sativa, Nipponbare strain, clone
RT OJ136E01, from chromosome 10, complete sequence.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC079632; AAL73569.1; -
DR EMBL; AC108883; AAM08628.1; -
DR InterPro; IPR005162; Retrotrans_gag.
DR Pfam; PF03732; Retrotrans_gag; 1.
KW Hypothetical protein: Polyprotein.
SQ
SEQUENCE 290 AA; 33370 MW; 93A623E60C8C5909 CRC64;

Query Match 15.1%; Score 68; DB 10; Length 290;
Best Local Similarity 36.4%; Pred. No. 4.6;
Matches 20; Conservative 8; Mismatches 23; Indels 4; Gaps 2;

QY 18 QANAEF--CPALVSEILDFPFISLEPLFKLSLAKFDAPP--EAVNAKLGVRKCTDQ 68
DB 66 QQNOQFGPPPSHVSKLDFLRIOPTFSSTNPMENDWLRAIEKLTITLQCNDQ 120

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Search completed: January 2, 2003, 14:55:18
 Job time : 32 secs

(HUMA-) HUMAN GENOME SCI INC.

XX Gentz RL, Ni J, Yu G;
 XX N-PSDB: AAT94831.
 DR WPI: 1997-480206/44.
 XX
 PT Human endometrial specific steroid-binding factor I, II and III -
 PT used to treat inflammation, asthma, rhinitis, cystic fibrosis,
 PT allergy disease, neoplasia, atopy etc.
 XX
 PS Claim 18; Page 63-64; 92pp; English.
 XX
 CC This sequence comprises human endometrial specific steroid binding
 CC factor II (ESF II), a protein that inhibits phospholipase A2
 CC activity, binds to polychlorinated biphenyl compounds, reduces
 CC foreign protein antigenicity, inhibits monocyte and neutrophil
 CC chemotaxis and phagocytosis, inhibits platelet aggregation,
 CC regulates eicosanoid levels in the human uterus and controls the
 CC growth of endometrial cells. The amino acid sequence was deduced
 CC from a cDNA clone (see AAT94831) derived from cycloheximide-treated
 CC CEM cells. ESF I (see AAW35802) and ESF III (see AAW35804) are also
 CC claimed. Human ESF II has about 49% identity with rat prostatic
 CC steroid-binding protein. Recombinant ESF I, II and III can be
 CC expressed in host cells for use in claimed methods (a) for treating
 CC a patient in need of ESF I, II or III (including expression of the
 CC polypeptide in vivo) and (b) for identifying compounds which bind
 CC to and inhibit activation of the ESF polypeptide. hESF I, II and
 CC II may be used to treat inflammation, asthma, rhinitis, cystic
 CC fibrosis, allergy disease, neoplasia and atopy.
 CC
 SQ Sequence 90 AA:
 Query Match 100.0%; Score 90; DB 19; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFAPPAVAAKL 60
 Db 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFAPPAVAAKL 60
 QY 61 GVKRCTDQMSLQKRSLAEVLVKILKKCSV 90
 Db 61 GVKRCTDQMSLQKRSLAEVLVKILKKCSV 90
 RESULT 2
 AAW59776
 ID AAW59776 standard; Protein: 90 AA.
 XX
 AC AAW59776;
 XX
 DT 12-OCT-1998 (first entry)
 XX
 DE Amino acid sequence of the human steroid binding protein C1.
 XX
 KW Human steroid-binding protein C1; hSBP1; hSBP2; breast cancer; probe;
 KW gene therapy vector; ribozyme; probe; hybridisation; amplification;
 KW antibody; immunoassay.
 XX
 OS Homo sapiens.
 XX
 PN W09821331-A1.
 XX
 PD 22-MAY-1998.
 XX
 PF 07-NOV-1997; 97WO-US20674.
 XX
 PR 12-NOV-1996; 96US-0747547.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Akerblom IE, Goli SK, Hawkins PR, Hillman JL, Murry LE;
 XX

DR WPI: 1998-297935/26.
 DR N-PSDB: AAW41579.
 XX
 PT New human steroid binding proteins C1 and C2 - useful for, e.g.
 PT diagnosis, monitoring and treating breast cancer, and for drug
 PT screening
 XX
 PS Claim 1; Fig 1; 70pp; English.
 XX
 CC This is the amino acid sequence of the human steroid-binding protein
 CC C1 (hSBP1) used in the method of the invention for the diagnosis,
 CC monitoring and treatment of breast cancer. hSBP1 and hSBP2 are useful
 CC as markers for breast cancer, i.e. measuring levels of hSBP1 and hSBP2
 CC used for diagnosis or monitoring the disease, to identify subjects
 CC at risk and to discriminate between different forms of cancer for
 CC selection of appropriate therapies. They may also be used for drug
 CC screening. Nucleic acids encoding hSBP1 and hSBP2 can be used in gene
 CC therapy vectors to overexpress the steroid-binding proteins, preventing
 CC binding of steroids, or antisense sequences, ribozymes. Their nucleic
 CC acids can also be used for the diagnosis and monitoring (by quantifying
 CC expression of hSBP), as source of probes for hybridisation and
 CC amplification of genomic or related sequences for studying regulation of
 CC gene function and for mapping the genomic sequence. Antibodies are used
 CC as diagnostic reagents in standard immunoassays for hSBP.
 CC
 SQ Sequence 90 AA:
 Query Match 100.0%; Score 90; DB 19; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFAPPAVAAKL 60
 Db 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFAPPAVAAKL 60
 QY 61 GVKRCTDQMSLQKRSLAEVLVKILKKCSV 90
 Db 61 GVKRCTDQMSLQKRSLAEVLVKILKKCSV 90
 RESULT 3
 AAW54271
 ID AAW54271 standard; Protein: 90 AA.
 XX
 AC AAW54271;
 XX
 DT 29-JUL-1998 (first entry)
 XX
 DE B0101 antigenic peptide epitope 1.
 XX
 KW B0101; breast cancer; diagnosis; prevention; treatment; gene therapy;
 KW immunisation; drug screening; epitope.
 XX
 OS Homo sapiens.
 XX
 PN W09807857-A1.
 XX
 PD 26-FEB-1998.
 XX
 PF 19-AUG-1997; 97WO-US14665.
 XX
 PR 15-AUG-1997; 97US-0912276.
 XX
 PR 19-AUG-1996; 96US-0697105.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;
 PI Gordon J, Granadosen, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI: 1998-169161/15.
 DR N-PSDB: AAV26461.
 XX

PT New Bu101 protein over-expressed in breast cancer - useful for, e.g.
 PT diagnosis, treatment and prevention of breast cancer

PS Claim 17; Page 90; 105pp; English.

XX This represents a Bu101 polypeptide sequence. Bu101 is a member of the
 CC uteroglobin family of proteins and is over-expressed in breast cancer.
 CC Cells transfected with a recombinant expression system comprising a
 CC sequence derived from the Bu101 open reading frame and with at least 50
 CC percent identity to the sequences shown in AAV26458 to AAV26461 are used
 CC to produce Bu101 polypeptides containing at least 1 epitope. These are
 CC used to detect Bu101-specific antibodies which are used correspondingly
 CC to detect Bu101 antigens. The Bu101 polynucleotide sequences can be used
 CC in a method for detecting the presence of a target Bu101 polynucleotide.
 CC The various assays are used for diagnosis, prognosis, staging, monitoring,
 CC monitoring, treating and preventing diseases of the breast (especially
 CC cancer and its metastases), and also for determining susceptibility. The
 CC Bu101 polypeptides are also useful in drug screening, e.g. to identify
 CC antagonists of Bu101, potentially useful therapeutically and as targets
 CC for therapy. The antibodies are also useful for targeted drug delivery
 CC and therapeutically to neutralise Bu101 polypeptides. Fragments of the
 CC Bu101 nucleic acid are useful as probes and primers, e.g. for detection
 CC of altered gene expression or in fluorescent in situ hybridisation, also
 CC in gene therapy to generate antisense or ribozyme molecules or for
 CC genetic immunisation.

XX Sequence 90 AA;

Query Match 100.0%; Score 90; DB 19; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFIISPEFLSLAKDPAPPAVAATL 60
 DB 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFIISPEFLSLAKDPAPPAVAATL 60
 OY 61 GVKRCTDQMSLOKRSLIAEVLVKILKCSV 90
 DB 61 GVKRCTDQMSLOKRSLIAEVLVKILKCSV 90

RESULT 4
 AAM89613
 ID AAM89613 standard; Protein; 90 AA.

XX AAM89613;

DT 25-MAR-1999 (first entry)

DE Endometrial steroid binding protein II.

KM Endometrial steroid binding protein II; ESBPII; cancer; detection;
 KM endometriosis; endometrial fibroid; mammary cancer.

OS Homo sapiens.

PN WO9856248-A1.

PD 17-DEC-1998.

PF 09-JUN-1998; 98WO-US12053.

PR 09-JUN-1997; 97US-0049015.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PI Schmidt CJ, Wang X;

DR MPI: 1999-080843/07.
 DR N-PSDB; AAX00069.

PT Treatment of endometrial cancer, mammary cancer, endometriosis or
 PT endometrial fibroids - comprises administering endometrial steroid

PT binding protein II antagonist

PS Disclosure; Page 13; 19pp; English.

XX A method has been developed for the treatment of endometrial cancer,
 CC mammary cancer, endometriosis or endometrial fibroids. The method
 CC comprises administering endometrial steroid binding protein II (ESBPII)
 CC antagonist. Also described in the present invention are: (1) a method
 CC for diagnosing the above mentioned diseases comprising analysing the
 CC abnormally high level of ESBPII polypeptide in cells, tissues and bodily
 CC fluids; and (2) a diagnostic method for the diseases described above
 CC comprising analysing the abnormally high or low transcription level of
 CC ESBPII in cells, tissues and bodily fluids. The methods can be used to
 CC diagnose, treat, and monitor the progression, remission or recurrence of
 CC abnormal cell growth, such as cancers, especially endometrial and
 CC mammary cancer, and endometriosis and endometrial fibroids. The present
 CC sequence represents ESBPII, from the present invention.

XX Sequence 90 AA;

Query Match 100.0%; Score 90; DB 20; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFIISPEFLSLAKDPAPPAVAATL 60
 DB 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFIISPEFLSLAKDPAPPAVAATL 60
 OY 61 GVKRCTDQMSLOKRSLIAEVLVKILKCSV 90
 DB 61 GVKRCTDQMSLOKRSLIAEVLVKILKCSV 90

RESULT 5
 AAB13787
 ID AAB13787 standard; Protein; 90 AA.

XX AAB13787;

DT 20-JUN-2001 (first entry)

DE Human Bu101.

KM Human; breast cancer; breast disease detection; mammaglobin;
 KM uteroglobin; Bu101; endometrial; cytostatic.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 53

FT /label= Leu /note= "Encoded by CTG in polymorphic variant"

PN WO200035950-A2.

PD 22-JUN-2000.

PF 20-DEC-1999; 99WO-US30489.

PR 18-DEC-1998; 98US-0215818.

PA (ABBO) ABBOTT LAB.

PI Colpitts TL, Russell JE;

DR MPI: 2000-442366/38.

PT Multimeric polypeptide antigen and antibody specific to the antigen are
 PT useful for diagnosing, detecting and treating breast cancer -

PS Claim 1; Page 124; 124pp; English.

CC BU101 is a member of the uteroglobin protein family. The present
CC sequence is the protein sequence for human BU101. The present
CC invention relates to a multimeric polypeptide antigen, which comprises
CC of the present sequence and mamaglobin polypeptide (AAB13786).
CC Mamaglobin is another uteroglobin protein. The presence of multimeric
CC polypeptide antigen in a test sample can be used as the basis for a test
CC to diagnose breast disease e.g. breast cancer, in a patient. The
CC detection can be carried out using antibodies specific for the multimeric
CC polypeptide antigen. The present sequence can either have a Pro or Leu
CC residue at position 53, since the coding sequence has a single
CC nucleotide T/C polymorphism at nucleotide position 254.
XX
SQ Sequence 90 AA:
Query Match 100.0%; Score 90; DB 21; Length 90;
Best Local Similarity 100.0%; Pred. No. 2,2e+82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAKL 60
DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAKL 60
OY 61 GVKRCTDQMSLQKRSLSLAIEVLVKILKCSV 90
DB 61 GVKRCTDQMSLQKRSLSLAIEVLVKILKCSV 90
RESULT 6
AAB07501
ID AAB07501 standard; Protein: 90 AA.
XX
AC AAB07501:
XX
DT 20-OCT-2000 (first entry)
XX
DE Amino acid sequence of a human BU101 polypeptide.
XX
KW Human; BU101; breast disease.
XX
OS Homo sapiens.
XX
PN WO200041516-A2.
XX
PD 20-JUL-2000.
XX
PE 19-JAN-2000; 2000WO-US01309.
XX
PR 19-JAN-1999; 99US-0233693.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-rapp L;
PI Russell JC, Scheffel CP, Stroupe SD;
XX
DR WPI: 2000-475906/41.
DR N-PSDB: AAA58880.
XX
PT Detecting presence of target BU101 polynucleotide in sample useful for
PT detection of breast cancer, comprises contacting sample with
PT BU101-specific polynucleotide and determining binding -
XX
PS Claim 23; Page 125; 127pp; English.
XX
CC The present sequence represents a BU101 polypeptide. The BU101 gene is
CC transcribed from breast tissue. The specification describes a method for
CC detecting the presence of a target BU101 polynucleotide in a test
CC sample. The method comprises contacting the sample with at least one
CC BU101-specific polynucleotide (AAA58875-80), and detecting bound
CC polynucleotides. The method and BU101 polynucleotides are useful for
CC detecting the presence of BU101 polynucleotides. The methods may be
CC used for the diagnosis of breast disease, indicated by the formation
CC of complexes.

XX
SQ Sequence 90 AA:
Query Match 100.0%; Score 90; DB 21; Length 90;
Best Local Similarity 100.0%; Pred. No. 2,2e+82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAKL 60
DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAKL 60
OY 61 GVKRCTDQMSLQKRSLSLAIEVLVKILKCSV 90
DB 61 GVKRCTDQMSLQKRSLSLAIEVLVKILKCSV 90
RESULT 7
AAB03768
ID AAB03768 standard; Protein: 90 AA.
XX
AC AAB03768:
XX
DT 06-OCT-2000 (first entry)
XX
DE Human endometrial specific steroid-binding factor II protein sequence.
XX
KW Endometrial specific steroid-binding factor; human; hESF; inflammation;
KW asthma; rhinitis; cystic fibrosis; air way disease; neoplasia; atopy;
KW elcosanoid level regulator; chemotaxis inhibitor; endometrial cancer; ss.
XX
OS Homo sapiens.
XX
PN US606724-A.
XX
PD 23-MAY-2000.
XX
PE 21-MAR-1997; 97US-0821451.
XX
PR 21-MAR-1996; 96US-0014724.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Yu G, Gentz R, NI J;
XX
DR WPI: 2000-375600/32.
DR N-PSDB: AAA59729.
XX
PT Novel gene encoding human endometrial specific steroid-binding factor
PT I, II and III which is useful for treating asthma, rhinitis, cystic
PT fibrosis, airway disease and neoplasia -
XX
PS Claim 1; Fig 2; 36pp; English.
XX
CC This invention relates to nucleic acid molecules encoding portions of the
CC human endometrial specific steroid-binding factors I, II, and III. Also
CC included in the invention are hESF I, II, and III polypeptide sequences.
CC The nucleotide sequence exhibit antihasthmatic, antiinflammatory,
CC antiallergic, and cytostatic properties. The polynucleotides are used in
CC gene therapy to express hESF I, II and III polypeptides in vivo to treat
CC and/or prevent inflammation, asthma, rhinitis, cystic fibrosis, air way
CC disease, neoplasia and atopy. The polynucleotides are also used to
CC inhibit phospholipase A2 activity, bind polychlorinated biphenyls, reduce
CC foreign protein antigenicity, inhibit monocyte and neutrophil chemotaxis
CC and phagocytosis, inhibit platelet aggregation, regulate elcosanoid
CC levels in the human uterus and control the growth of endometrial cells.
CC The polynucleotides are also useful for detecting complementary
CC polynucleotides as a diagnostic reagent. The hESF I, II and III
CC polynucleotides are used to detect complementary polynucleotides such as
CC a diagnostic reagent. Detection of a mutated form of hESF I, II and III
CC associated with a dysfunction will provide a diagnostic tool that can
CC define diagnosis of a disease or susceptibility to a disease which
CC results from under-expression, over-expression or altered expression of
CC hESF I, II and III e.g. a susceptibility to inherited asthma and

CC endometrial cancer. They are also useful for chromosome identification.
CC The present sequence represents a hsp70 protein sequence identified in
CC the invention.
XX
SQ Sequence 90 AA:
Query Match 100.0%; Score 90; DB 21; Length 90;
Best local similarity 100.0%; Pred. No. 2.2e-82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MKLSVCLLVLTALCCYQANAEECPALVSELDFFFISEPLFKLSLAKDPAPPEAFAAKL 60
DB 1 MKLSVCLLVLTALCCYQANAEECPALVSELDFFFISEPLFKLSLAKDPAPPEAFAAKL 60
OY 61 GVARCTDOMSLQKRSLSIAEVLVKILKCSV 90
DB 61 GVARCTDOMSLQKRSLSIAEVLVKILKCSV 90
RESULT 8
AA84875
ID AA84875 standard; Protein; 90 AA.
XX
AC AA84875;
XX
DT 08-AUG-2000 (first entry)
XX
DE A human endometrial specific steroid-binding protein II.
XX
KW Human; endometrial specific steroid-binding protein II; ESBP11;
KW breast tumour; prostate cancer; gynaecological cancer; cancer;
KW endometrial cancer; ovarian cancer; uterine cancer.
XX
OS Homo sapiens.
XX
PN WO200020043-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US232352.
XX
PR 05-OCT-1998; 98US-0103093.
XX
PA (DIAD-) DIADENUS LLC.
XX
PI Macina RA;
XX
DR WPI: 2000-303648/26.
DR N-PSDB: AAA14953.
XX
PT Diagnosing, staging, monitoring, imaging and treating prostate and
PT gynaecological cancers by measuring levels of endometrial specific
PT steroid-binding protein (ESBP)II expression
XX
PS Claim 6; Page 31-32; 35pp; English.
XX
CC The present sequence represents a human endometrial specific steroid-
CC binding protein (ESBP) II. The ESBP11 protein is overexpressed in
CC breast tumours. The specification describes a method for diagnosing
CC prostate or a gynaecological cancer. The method comprises measuring
CC levels of ESBP11 in cells, tissues or body fluids of a patient, and
CC comparing this to levels from a normal control, where a variance in
CC levels indicates cancer. The method is used to diagnose, stage, monitor,
CC image or treat prostate or gynaecological cancer. The gynaecological
CC cancers include breast, endometrial, ovarian and uterine cancer.
XX
SQ Sequence 90 AA:
Query Match 100.0%; Score 90; DB 21; Length 90;
Best local similarity 100.0%; Pred. No. 2.2e-82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MKLSVCLLVLTALCCYQANAEECPALVSELDFFFISEPLFKLSLAKDPAPPEAFAAKL 60

DB 1 MKLSVCLLVLTALCCYQANAEECPALVSELDFFFISEPLFKLSLAKDPAPPEAFAAKL 60
OY 61 GVARCTDOMSLQKRSLSIAEVLVKILKCSV 90
DB 61 GVARCTDOMSLQKRSLSIAEVLVKILKCSV 90
RESULT 9
AAG5989
ID AAG5989 standard; Protein; 90 AA.
XX
AC AAG5989;
XX
DT 11-FEB-2002 (first entry)
XX
DE Lipophilin B polypeptide.
XX
KW Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
KW cancer; B726P; Lipophilin B; mammaglobin.
XX
OS Homo sapiens.
XX
PN WO200175171-A2.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001WO-US10631.
XX
PR 03-APR-2000; 2000US-194241P.
PR 20-JUL-2000; 2000US-219862P.
PR 27-JUL-2000; 2000US-221300P.
PR 18-DEC-2000; 2000US-256582P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Houghton RL, Dillon DC, Moles DA, Xu J, Zehentner B, Persing DH;
PI WPI: 2001-626449/72.
XX
DR N-PSDB: AAI67269.
XX
PF Identifying tissue (tumour)-specific polynucleotides overexpressed in
PF tissue of interest as compared to control tissue, for detecting cancer
PF cells in patient, comprises DNA microarray analysis or quantitative
PF polymerase chain reaction
XX
PS Examples; Page 127; 127pp; English.
XX
CC The invention relates to identifying tissue-specific polynucleotides (P)
CC that involves performing a genetic subtraction to identify pool of (P)
CC from tissue of interest (TI), performing DNA microarray analysis to
CC identify first subset of polynucleotides (SPI) at least 2-fold over
CC expressed in TI, and performing quantitative polymerase chain reaction
CC (PCR) analysis on SPI to identify second subset of (P). The method is
CC useful for determining the presence or absence of a cancer cell in a
CC patient, monitoring the progression of cancer in a patient using a
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
CC urine or a tumour biopsy sample. The methods are useful for determining
CC the presence or absence of or monitoring progression of prostate, breast,
CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
CC sequence represents the lipophilin B polypeptide.
XX
SQ Sequence 90 AA:
Query Match 100.0%; Score 90; DB 22; Length 90;
Best local similarity 100.0%; Pred. No. 2.2e-82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MKLSVCLLVLTALCCYQANAEECPALVSELDFFFISEPLFKLSLAKDPAPPEAFAAKL 60
DB 1 MKLSVCLLVLTALCCYQANAEECPALVSELDFFFISEPLFKLSLAKDPAPPEAFAAKL 60

QY 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90
 DB 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90

RESULT 10

AAE07518
 ID AAE07518 standard; Protein: 90 AA.

AC AAE07518:

DT 06-NOV-2001 (first entry)

DE Human lipophilin B protein.

KW Human: lipophilin B; cytosolic; vaccine; gene therapy; uteroglobin;

KM cancer; breast; ovary; prostate.

OS Homo sapiens.

PN WO200158947-A1.

PD 16-AUG-2001.

PF 08-FEB-2001; 2001WO-US04439.

PR 11-FEB-2000; 2000US-0183495.

PR 28-JUN-2000; 2000US-0215735.

PA (CORI-) CORIXA CORP.

PI Carter D, Vedvick TS, Vallieve-Douglass J, Houghton RL, Dillon DC;

DR WPI: 2001-497069/54.

DR N-PSDB: AAD13756.

PT Novel isolated complex two lipophilin-like polypeptides linked by at

PT least one disulphide bond, used to treat or prevent breast, ovarian or

PS prostate cancer -

PS Example 5; Page 72; 91pp; English.

CC The invention relates to a complex comprising a lipophilin-like

CC polypeptide linked by at least one disulphide bond to a second

CC lipophilin-like polypeptide. Lipophilin-like protein are members of

CC uteroglobin superfamily. Lipophilin-like proteins are useful in the

CC preparation of vaccines. The complex containing lipophilin-like

CC proteins are useful for treating or preventing breast, ovarian or

CC prostate cancer. The complex is also used for determining the

CC presence or absence of cancer in a patient, or monitor the progress

CC of cancer in a patient. Lipophilin DNA is also useful in gene therapy.

CC The present sequence is human lipophilin B protein.

CC

DB 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90

RESULT 11

AAAB31681

ID AAB31681 standard; Protein: 90 AA.

AC AAB31681:

XX 30-APR-2001 (first entry)

DT An endometrial specific steroid binding factor II.

XX

KW Human; endometrial specific steroid binding factor; hESF; hESFI; hESFII;

OS Homo sapiens.

PF Key Location/Qualifiers

FT Peptide 1..21

PN US6174992-B1.

PD 16-JAN-2001.

PF 08-MAR-1999; 99US-0263810.

PR 21-MAR-1996; 96US-0014724.

PR 21-MAR-1997; 97US-0821451.

PA (HUMA-) HUMAN GENOME SCI INC.

PI NI J, Yu G, Gentz R;

DR WPI: 2001-158477/16.

DR N-PSDB: AAF25213.

PT New human endometrial specific steroid binding factors, useful for

PT treating and preventing inflammation, asthma, rhinitis, cystic

PT fibrosis, airway disease, neoplasia and atopy

PS Claim 1; Fig 2; 36pp; English.

CC The present sequence represents a human endometrial specific steroid

CC binding factor (hESF). The specification describes hESFI, hESFII, and

CC hESFIII. hESFI, II and III polypeptides, and polynucleotides encoding

CC them are useful for treating and preventing inflammation, asthma,

CC rhinitis, cystic fibrosis, airway disease, neoplasia and atopy,

CC inhibiting phospholipase A2 activity, binding polychlorinated

CC biphenyls, reducing foreign protein antigenicity, inhibiting monocyte

CC and neutrophil chemotaxis and phagocytosis, inhibiting platelet

CC aggregation, regulating eicosanoid levels in the human uterus, and for

CC controlling the growth of endometrial cells. hESF polypeptides and

CC nucleotides are also useful for research, biological, clinical or

CC therapeutic purposes.

XX

RESULT 12

ABB09634

ID ABB09634 standard; Protein: 90 AA.

AC ABB09634:

DT 29-MAY-2002 (first entry)

[illegible]

KW inhibin, chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritic; haemostatic; antiatherosclerotic;
 KW cytosstatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
 KW antifungal; vulnereary; antitlcer.
 XX
 OS Homo sapiens.
 PN WO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US03800.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 XX 27-APR-2000; 2000US-0560875.
 XX
 PA (HXS-) HXSQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-457740/49.
 XX N-PSDB; ABA09151.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX
 PS Claim 20: Page 275; 1963pp; English.
 XX
 CC Sequences ABB10981-ABB12330 represent 1310 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides,
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g. by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g. asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g. osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g. of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.

```

XX Sequence 117 AA;
SQ
Query Match 100.0%; Score 90; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8e-82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVTLALCCYQOANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 60
DB 28 MKLSVCLLVTLALCCYQOANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 87
QY 61 GVKRCTDOMSLQKRSLIAEVLVKILKCSV 90
DB 88 GVKRCTDOMSLQKRSLIAEVLVKILKCSV 117

RESULT 14
AAV48606
ID AAY48606 standard; Protein: 120 AA.
AC AAY48606;
DE 08-DEC-1999 (first entry)
DE Human breast tumour-associated protein 67.
KW Expressed sequence tag; EST; human; breast; cancer; gene therapy;
KW treatment; tumour; cytostatic; medicament.
XX Homo sapiens.
XX DE19813839-A1.
XX 23-SEP-1999.
XX 20-MAR-1998; 98DE-1013839.
XX 20-MAR-1998; 98DE-1013839.
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX WPI; 1999-528981/45.
XX N-PSDB; AAZ33666.
XX
PT Human nucleic acid sequences and protein products from tumor breast
PT tissue, useful for breast cancer therapy -
XX
PS Claim 22; 172; 188bp; German.
CC This invention describes novel human nucleic acid sequences from tumor
CC breast tissue which have cytostatic activity. The nucleic acid sequences
CC can be used to produce and isolate full-length gene sequences. They can
CC be used to express proteins, which can be used as tools to find an
CC actively against breast cancer. The sequences can be used in sense or
CC antisense form. They are especially useful for medicaments for gene
CC therapy to treat breast cancer. AAY48540-Y48617 represent protein
CC fragments encoded by the expressed sequence tags described in the method
CC of the invention.
XX
SQ Sequence 120 AA;
Query Match 100.0%; Score 90; DB 20; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.8e-82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVTLALCCYQOANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 60
DB 31 MKLSVCLLVTLALCCYQOANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 90
QY 61 GVKRCTDOMSLQKRSLIAEVLVKILKCSV 90

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DB 91 GVKRCTDOMSLQKRSLIAEVLVKILKCSV 120

RESULT 15
AAO20554
ID AAO20554 standard; Protein: 89 AA.
XX
XX AAO20554;
AC
DE 27-JUN-2002 (first entry)
DE Protein of human Lipophilin B.
DE Immunogenic epitope; hormonally regulated organ; malignant tumour;
KW Lipophilin; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX MISC-difference 11 /label= Lys
XX FT /note="Encoded by AGC"
XX
XX US2002034739-A1.
XX 21-MAR-2002.
XX
XX 07-JUL-1998; 98US-0110716.
XX 07-JUL-1998; 98US-0110716.
XX
XX (LEHR/) LEHRER R I.
XX (ZHAO/) ZHAO C.
XX (GLAS/) GLASGOW B J.
XX
XX Lehrer RI, Zhao C, Glasgow BJ;
XX WPI; 2002-338922/37.
XX N-PSDB; AAK99491.
XX
PT Peptides having the sequence of human lipophilin A, B and C are
PT associated with carcinomas of hormonally regulated organs and are
PT useful in the diagnosis and prognosis of various cancers -
XX
PS Claim 7; Fig 5; 22pp; English.
CC The invention relates to a peptide comprising the amino acid sequences of
CC human lipophilin A, B, or C or its allelic variant or fragment comprising
CC at least one immunogenic epitope, which is purified and isolated, and may
CC have the N-terminal acylated and/or C-terminal amidated or be a fusion
CC protein. Molecules of the invention are used in the diagnosis and
CC prognosis of malignant tumours associated with hormonally regulated
CC organs such as uterus, ovary, prostate, testis, breast, kidney and
CC thymus. This sequence represents the human Lipophilin B protein of the
CC invention.
XX
SQ Sequence 89 AA;
Query Match 87.8%; Score 79; DB 23; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.2e-71;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LALCCYQOANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKLGVKRCTDOMSL 71
DB 11 LALCCYQOANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKLGVKRCTDOMSL 70
QY 72 QKRSLIAEVLVKILKCSV 90
DB 71 QKRSLIAEVLVKILKCSV 89

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Job time : 36 secs

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Run on: January 2, 2003, 14:55:22 ; Search time 11 Seconds

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Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	450	100.0	90	10	US-09-110-716-29
3	450	100.0	90	10	US-09-934-054-1
4	450	100.0	90	10	US-09-985-911-4
5	342	76.0	69	10	US-09-110-716-37
6	277	61.6	90	10	US-09-985-911-2
7	268	59.6	90	10	US-09-110-716-27
8	246	54.7	50	10	US-09-864-761-44240
9	238	52.9	83	9	US-09-982-598-260
10	238	52.9	83	9	US-09-989-2934-260
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12	238	52.9	83	9	US-09-990-444-260
13	238	52.9	83	9	US-09-989-730-260
14	238	52.9	83	9	US-09-990-436-260
15	238	52.9	83	9	US-09-991-181-260
16	238	52.9	83	9	US-09-993-687-260
17	238	52.9	83	10	US-09-989-722-260
18	238	52.9	83	10	US-09-989-723-260
19	238	52.9	83	10	US-09-989-279-260

20	238	52.9	83	10	US-09-989-721-260	Sequence 260, App
21	238	52.9	83	10	US-09-989-731-260	Sequence 260, App
22	238	52.9	83	10	US-09-989-731-260	Sequence 260, App
23	238	52.9	83	10	US-09-991-071-260	Sequence 260, App
24	238	52.9	83	10	US-09-990-441-260	Sequence 260, App
25	238	52.9	83	10	US-09-991-161-260	Sequence 260, App
26	238	52.9	83	10	US-09-993-604-260	Sequence 260, App
27	238	52.9	83	10	US-09-990-451-260	Sequence 260, App
28	238	52.9	83	10	US-09-989-721-260	Sequence 260, App
29	206	45.8	111	10	US-09-934-051-5	Sequence 5, Appl1
30	202	44.9	90	10	US-09-985-911-25	Sequence 25, Appl1
31	202	44.9	90	10	US-09-985-911-26	Sequence 26, Appl1
32	172	38.2	69	10	US-09-110-715-12	Sequence 12, Appl1
33	172	38.2	69	10	US-09-110-715-36	Sequence 36, Appl1
34	171	38.0	112	10	US-09-934-051-8	Sequence 8, Appl1
35	142	31.6	74	10	US-09-110-715-35	Sequence 35, Appl1
36	111	24.7	74	10	US-09-110-715-38	Sequence 38, Appl1
37	102	22.7	91	10	US-09-934-054-9	Sequence 9, Appl1
38	91	20.2	105	10	US-09-768-826-47	Sequence 47, Appl1
39	75.5	16.8	93	9	US-10-081-817-32	Sequence 32, Appl1
40	75.5	16.8	93	12	US-10-052-586-244	Sequence 244, App
41	64.5	14.3	100	10	US-09-867-550-1430	Sequence 1430, App
42	62	13.8	178	10	US-09-969-834-1	Sequence 1, Appl1
43	59.5	13.2	95	10	US-09-925-299-1494	Sequence 1494, App
44	58	12.9	162	10	US-09-747-155-339	Sequence 339, App
45	58	12.9	226	9	US-09-895-913A-362	Sequence 362, App

ALIGNMENTS

```

RESULT 1
US-09-825-301-77
; Sequence 77, Application US/09825301
; Patent No. US2002009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; OF INVENTION: AND MONITORING OF BREAST CANCER
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-301-77

Query Match      100.0%; Score 450; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.1e-45;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFSEPLFKSLKFPDAPPAVAKL 60
Db      1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFSEPLFKSLKFPDAPPAVAKL 60

QY      61 GVKRCTDQMSLQKRSLLAEVLYKIKKCSV 90
Db      61 GVKRCTDQMSLQKRSLLAEVLYKIKKCSV 90

RESULT 2
US-09-110-716-29
; Sequence 29, Application US/09110716A
; Patent No. US20020034739A1
; GENERAL INFORMATION:

```

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; APPLICANT: Lehrer, Robert I.
; APPLICANT: Zhao, Chengquan
; APPLICANT: Glasgow, Benjamin J.
; TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
; FILE REFERENCE: 22000-20596.00
; CURRENT APPLICATION NUMBER: US/09/110,716A
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 90
; TYPE: PRT
; ORGANISM: lipophilin B
US-09-110-716-29

Query Match          100.0%; Score 450; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,1e-45;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAAKL 60
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DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAAKL 60
    |||||||

QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
    |||||||
DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
    |||||||

RESULT 3
US-09-934-054-1
; Sequence 1, Application US/09934054
; Patent No. US20020107385A1
; GENERAL INFORMATION:
; APPLICANT: Akerblom, Ingrid E.
; Hillman, Jennifer L.
; Murry, Lynn E.
; Goll, Surya K.
; Hawkins, Phillip R.
; TITLE OF INVENTION: BREAST TUMOR SPECIFIC PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025-6936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/934,054
; FILING DATE: 21-Aug-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,547
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0077 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: <unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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US-09-934-054-1

Query Match          100.0%; Score 450; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,1e-45;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAAKL 60
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DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAAKL 60
    |||||||

QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
    |||||||
DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
    |||||||

RESULT 4
US-09-985-911-4
; Sequence 4, Application US/09985911
; Patent No. US20020151012A1
; GENERAL INFORMATION:
; APPLICANT: NI ET AL.
; TITLE OF INVENTION: HUMAN ENDOMETRIAL SPECIFIC STEROID-BINDING FACTOR I, II AND II
; FILE REFERENCE: PR25703
; CURRENT APPLICATION NUMBER: US/09/985,911
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/583,169
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/263,810
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 08/821,451
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: 60/014,724
; PRIOR FILING DATE: 1996-03-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: human
US-09-985-911-4

Query Match          100.0%; Score 450; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,1e-45;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAAKL 60
    |||||||
DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAAKL 60
    |||||||

QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
    |||||||
DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
    |||||||

RESULT 5
US-09-110-716-37
; Sequence 37, Application US/09110716A
; Patent No. US20020034739A1
; GENERAL INFORMATION:
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Zhao, Chengquan
; APPLICANT: Glasgow, Benjamin J.
; TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
; FILE REFERENCE: 22000-20596.00
; CURRENT APPLICATION NUMBER: US/09/110,716A
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Lgmb
US-09-110-716-37

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Query Match	76.0%;	Score 342;	DB 10;	Length 69;
Best Local Similarity	100.0%;	Pred. No. 2.8e-33;		
Matches 69;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy 22 EFCPALVSELDFFFISEPLFKLSLAKFDPAPPEAAVAKLGVCRCCTDQMSLQKRSLAEVL 81
|||||
Db 1 EFCPALVSELDFFFISEPLFKLSLAKFDPAPPEAAVAKLGVCRCCTDQMSLQKRSLAEVL 600

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QY      82 VKILKCSV 90
          |||||
Db      61 VKILKCSV 69
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RESULT 6
US-09-985-911-2
: Sequence 2, Application US/09985911
: Patent No. US20020151012A1
: GENERAL INFORMATION:
: APPLICANT: NI ET AL.
: TITLE OF INVENTION: HUMAN ENDOMETRIAL SPECIFIC STEROID-BINDING FACTOR I, II AND III
: FILE REFERENCE: PP257D3
: CURRENT APPLICATION NUMBER: US/09/985,911
: CURRENT FILING DATE: 2001-11-06
: PRIOR APPLICATION NUMBER: 09/583,169
: PRIOR FILING DATE: 2000-05-30
: PRIOR APPLICATION NUMBER: 09/263,810
: PRIOR FILING DATE: 1999-03-08
: PRIOR APPLICATION NUMBER: 08/821,451
: PRIOR FILING DATE: 1997-03-21
: PRIOR APPLICATION NUMBER: 60/014,724
: PRIOR FILING DATE: 1996-03-21
: NUMBER OF SEQ ID NOS: 27
: SOFTWARE: Patentin version 3.1
: SEQ ID NO 2
: LENGTH: 90
: TYPE: PRT
: ORGANISM: human
: US-09-985-911-2

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[illegible]

RESULT 7
 US-09-110-716-27
 : Sequence 27, Application US/09110716A
 : Patent No. US20020034739A1
 : GENERAL INFORMATION:
 : APPLICANT: Lehrer, Robert I.
 : APPLICANT: Zhao, Chengquan
 : APPLICANT: Glasgow, Benjamin J.
 : TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
 : FILE REFERENCE: 22000-20566.00
 : CURRENT APPLICATION NUMBER: US/09/110,716A
 : CURRENT FILING DATE: 1998-07-07
 : NUMBER OF SEQ ID NOS: 41
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 27
 : LENGTH: 90
 : TYPE: prt
 : ORGANISM: lipophilin A
 : US-09-110-716-27

Query	Match	Similarity	Score	CB	Length
Best	Local	Similarity	60.2%	Pred. No. 1.6e-24;	
Matches	53;	Conservative	12;	Mismatches	23;
				Indels	0;
				Gaps	0.

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1      RESULT 8
2      US-09-864-761-44240
3      Sequence 44240 Application US/09864761
4      Patent No. US20020048763A1
5      GENERAL INFORMATION:
6      APPLICANT: Penn, Sharon G.
7      APPLICANT: Rank, David R.
8      APPLICANT: Hanzel, David K.
9      APPLICANT: Chen, Wensheng
10     TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
11     FILE REFERENCE: Aecomica-X-1
12     FILE REFERENCE: Aecomica-X-1
13     CURRENT FILING DATE: 2001-05-23
14     CURRENT FILING DATE: 2001-05-23
15     PRIOR APPLICATION NUMBER: US 60/180,312
16     PRIOR APPLICATION NUMBER: US 60/207,456
17     PRIOR APPLICATION NUMBER: US 60/207,456
18     PRIOR FILING DATE: 2000-05-26
19     PRIOR APPLICATION NUMBER: US 09/632,386
20     PRIOR FILING DATE: 2000-08-03
21     PRIOR APPLICATION NUMBER: GB 24263.6
22     PRIOR FILING DATE: 2000-10-04
23     PRIOR APPLICATION NUMBER: US 60/236,359
24     PRIOR FILING DATE: 2000-09-27
25     PRIOR APPLICATION NUMBER: PCT/US01/00666
26     PRIOR FILING DATE: 2001-01-30
27     PRIOR APPLICATION NUMBER: PCT/US01/00667
28     PRIOR FILING DATE: 2001-01-30
29     PRIOR APPLICATION NUMBER: PCT/US01/00664
30     PRIOR FILING DATE: 2001-01-30
31     PRIOR APPLICATION NUMBER: PCT/US01/00669
32     PRIOR FILING DATE: 2001-01-30
33     PRIOR APPLICATION NUMBER: PCT/US01/00665
34     PRIOR FILING DATE: 2001-01-30
35     PRIOR APPLICATION NUMBER: PCT/US01/00668
36     PRIOR FILING DATE: 2001-01-30
37     PRIOR APPLICATION NUMBER: PCT/US01/00663
38     PRIOR FILING DATE: 2001-01-30
39     PRIOR APPLICATION NUMBER: PCT/US01/00662
40     PRIOR FILING DATE: 2001-01-30
41     PRIOR APPLICATION NUMBER: PCT/US01/00661
42     PRIOR FILING DATE: 2001-01-30
43     PRIOR APPLICATION NUMBER: PCT/US01/00670
44     PRIOR FILING DATE: 2001-01-30
45     PRIOR APPLICATION NUMBER: US 60/234,687
46     PRIOR FILING DATE: 2000-09-21
47     PRIOR APPLICATION NUMBER: US 09/608,408
48     PRIOR FILING DATE: 2000-06-30
49     PRIOR APPLICATION NUMBER: US 09/774,203
50     PRIOR FILING DATE: 2001-01-29
51     NUMBER OF SEQ ID NOS: 49117
52     SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
53     SEQ ID NO 44240
54     LENGTH: 50
55     TYPE: PRT
56     ORGANISM: Homo sapiens
57     FEATURE:
58     OTHER INFORMATION: MAP TO AC004127.1 SIGNAL = 1
59     OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
60     OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EST_HUMAN HIT: AM103293.1, EVALUATE 5.00e-21
OTHER INFORMATION: SWISSPROT HIT: O95969, EVALUATE 4.00e-22
US-09-864-761-44240

Query Match 54.7% Score 246; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 LDEFFISEPLFKLSLAKFDAPPEAVAKLGVRCTDQMSLOKRSLSIAEVL 81
Db 1 LDEFFISEPLFKLSLAKFDAPPEAVAKLGVRCTDQMSLOKRSLSIAEVL 50

RESULT 9
US-09-992-598-260

Sequence 260, Application US/09992598
Patent No. US20020160384A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerltzen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Kijavlin, Ivar L.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paonl, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC20

CURRENT APPLICATION NUMBER: US/09/992,598

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
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PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907

PRIOR FILING DATE:	1998-06-02
PRIOR APPLICATION NUMBER:	60/0878821
PRIOR FILING DATE:	1998-06-03
PRIOR APPLICATION NUMBER:	60/0880211
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PRIOR APPLICATION NUMBER:	60/0880252
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PRIOR APPLICATION NUMBER:	60/089801
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089907
PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089908
PRIOR FILING DATE:	1998-06-18

PRIOR APPLICATION NUMBER:	60/089947
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089948
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089952
PRIOR FILING DATE:	1998-06-19
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PRIOR FILING DATE:	1998-06-22
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PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090254
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090349
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PRIOR APPLICATION NUMBER:	60/090429
PRIOR FILING DATE:	1998-06-24
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PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090435
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090444
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090445
PRIOR FILING DATE:	1998-06-24
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PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090557
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090676
PRIOR FILING DATE:	1998-06-25
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PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090694
PRIOR FILING DATE:	1998-06-25
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PRIOR FILING DATE:	1998-06-25
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PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/090863
PRIOR FILING DATE:	1998-06-26
PRIOR APPLICATION NUMBER:	60/091360
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091478
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091633
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091978
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/091982
PRIOR FILING DATE:	1998-07-07
PRIOR APPLICATION NUMBER:	60/092182
PRIOR FILING DATE:	1998-07-09

Query Match	52.9%;	Score 238;	DB 9;	Length 83;
Best Local Similarity	60.8%;	Pred. No. 4.4e-21;		

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Matches 45; Conservative 13; Mismatches 16; Indels 0; Gaps 0;
QY 1 MKSVCLLTALCCQAARCPALVSELLDFPFSELPFKISLAKFPAPPEAVAKL 60
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MRLSVCLLWALACCCQAALVCPAVASEITVFLFLSDAVALNQLVAKLPPEALAKL 60
QY 61 GVKRCTDMSLOKR 74
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 EVKHCTDQISFKKR 74

RESULT 11
US-09-989-735-260
; Sequence 260, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P27301C61
; CURRENT APPLICATION NUMBER: US/09/989,735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 52.9%; Score 238; DB 9; Length 83;

Best Local Similarity 60.8%; Pred. No. 4.4e-21;
Matches 45; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELLDFFFISEPLFKLSLAKFDAPPEAVAAKL 60

DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSEIVTFLEISDAAVNLGVAKINPPEALAAKL 60
QY 61 GVKRCTDOMSLQKR 74
DB 61 EVKHCTDQISFKKR 74

RESULT 12
US-09-990-444-260

Sequence 260, Application US/09990444
Publication No. US20020193300A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Godowski, Paul J.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC19
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR FILING DATE: 1998-07-09

Query Match 52.9%; Score 238; DB 9; Length 83;

Best Local Similarity 60.8%; Pred. No. 4.4e-21;

Matches 45; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 MKLSVCLLVTTALCCYQANAEFCPALVSELIFFFTISEPLFKLSLAKTDAPEAVAAKL 60
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OY 61 GVKRCTDQMSLOKR 74
|||:|:
Db 61 EVKHTDQISFKR 74

RESULT 13
US-09-989-730-260
Sequence 260, Application US/09989730
Publication No. US20020197674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Napier, Mary A.
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APPLICANT: Paoni, Nicholas F.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 52.9%; Score 238; DB 9; Length 83;
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QY 61 GVKRCTQMSLQKR 74
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RESULT 15

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; Sequence 260, Application US/09991181
; Publication No. US20020197615A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC53
; CURRENT APPLICATION NUMBER: US/09/991,181
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 52.9%; Score 238; DB 9; Length 83;
Best Local Similarity 60.8%; Pred. No. 4.4e-21;
Matches 45; Conservatively 13; Mismatches 16; Indels 0; Gaps 0;

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 Job time : 12 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2003, 14:59:13 ; Search time 15 Seconds

(without alignments)
176.538 Million cell updates/sec

Title: US-09-806-301-2

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	90	100.0	90	4 US-09-583-169-4	Sequence 4, Appl1
5	90	100.0	90	4 US-09-215-818-6	Sequence 6, Appl1
6	69	76.7	69	4 US-08-912-276-23	Sequence 23, Appl1
7	45	50.0	45	4 US-08-912-276-22	Sequence 22, Appl1
8	22	24.4	22	4 US-08-912-276-21	Sequence 21, Appl1
9	15	16.7	15	4 US-08-912-276-16	Sequence 16, Appl1
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45	6	6.7	22	1 US-07-965-663A-20	Sequence 20, Appl1

ALIGNMENTS

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; Patent No. 6066724
; GENERAL INFORMATION:
; APPLICANT: Jian NI, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; TITLE OF INVENTION: Binding Factor I, II and III
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
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; APPLICATION NUMBER: US/08/821,451A
; FILING DATE: March 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,724
; FILING DATE: March 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1744
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 AMINO ACIDS
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; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-821-451A-4
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Db 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFIISPLFKLSLAKFDAPPEAAVAKL 60
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Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 2
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; Sequence 4, Application US/09263810
; Patent No. 6174992
; GENERAL INFORMATION:
; APPLICANT: Jian NI, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
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; LENGTH: 90 AMINO ACIDS
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; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
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RESULT 3
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; Patent No. 6183952
; GENERAL INFORMATION:
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice

APPLICANT: Colpits, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Gordon, Julian
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klass, Michael R.
; APPLICANT: Kratochvil, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Russell, John C.
; APPLICANT: Stroupe, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,276
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5972.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6183952e
; US-08-912-276-15

Query Match 100.0%; Score 90; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.4e-80;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFIISPLFKLSLAKFDAPPEAAVAKL 60
|||||
Db 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFIISPLFKLSLAKFDAPPEAAVAKL 60
OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
|||||
Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 4
US-09-583-169-4
; Sequence 4, Application US/09583169
; Patent No. 6338948
; GENERAL INFORMATION:
; APPLICANT: Jian NI, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

```

ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/583,169
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/821,451
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-583-169-4

Query Match          100.0%; Score 90; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.4e-80;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQNAEPCPALVSELDFFFI SEPLFKLSLAKDPAPPAVAATL 60
DB 1 MKLSVCLLVLTALCCYQNAEPCPALVSELDFFFI SEPLFKLSLAKDPAPPAVAATL 60

QY 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSY 90
DB 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSY 90

RESULT 5
US-09-215-818-6
Sequence 6, Application US/09215818A
Patent No. 6379671
GENERAL INFORMATION:
APPLICANT: Colpitts, Tracey
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
FILE REFERENCE: 5972, US P2
CURRENT APPLICATION NUMBER: US/09/215,818A
FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/912,276
EARLIER FILING DATE: 1997-08-17
EARLIER APPLICATION NUMBER: 08/697,105
EARLIER FILING DATE: 1996-08-19
EARLIER APPLICATION NUMBER: 08/912,149
EARLIER FILING DATE: 1997-08-15
EARLIER APPLICATION NUMBER: 08/697,106
EARLIER FILING DATE: 1996-08-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 90
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-215-818-6
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```

Query Match          100.0%; Score 90; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.4e-80;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQNAEPCPALVSELDFFFI SEPLFKLSLAKDPAPPAVAATL 60
DB 1 MKLSVCLLVLTALCCYQNAEPCPALVSELDFFFI SEPLFKLSLAKDPAPPAVAATL 60

QY 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSY 90
DB 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSY 90

RESULT 6
US-08-912-276-23
Sequence 23, Application US/08912276
Patent No. 6183952
GENERAL INFORMATION:
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colpitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Gordon, Julian
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Stroupe, Steven D.
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5972, US P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6183952e
US-08-912-276-23

Query Match          76.7%; Score 69; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 6.2e-60;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 22 EECPALVSELDFFFIISPLFKLSLAKFDAPPEAVAAKLGVRCTDQMSLOKRSLIAEVL 81
|||||
DB 1 EECPALVSELDFFFIISPLFKLSLAKFDAPPEAVAAKLGVRCTDQMSLOKRSLIAEVL 60
OY 82 VKILKCSV 90
|||||
DB 61 VKILKCSV 69

RESULT 7

US-08-912-276-22
; Sequence 22, Application US/08912276
; Patent No. 6183952
; GENERAL INFORMATION:
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colpits, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Gordon, Julian
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klass, Michael R.
; APPLICANT: Kratochvil, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Russell, John C.
; APPLICANT: Stroupe, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912.276
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5972.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TEXES:
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6183952e
US-08-912-276-22

Query Match 50.0%; Score 45; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.9e-37;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 46 LAKFDAPPEAVAAKLGVRCTDQMSLOKRSLIAEVLVKILKCSV 90
|||||
DB 1 LAKFDAPPEAVAAKLGVRCTDQMSLOKRSLIAEVLVKILKCSV 45

RESULT 8

US-08-912-276-21
; Sequence 21, Application US/08912276
; Patent No. 6183952
; GENERAL INFORMATION:
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colpits, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Gordon, Julian
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klass, Michael R.
; APPLICANT: Kratochvil, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Russell, John C.
; APPLICANT: Stroupe, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912.276
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5972.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TEXES:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6183952e
US-08-912-276-21

Query Match 24.4%; Score 22; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.6e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 MSLOKRSLIAEVLVKILKCSV 90
|||||
DB 1 MSLOKRSLIAEVLVKILKCSV 22

RESULT 9

US-08-912-276-16
; Sequence 16, Application US/08912276
; Patent No. 6183952
; GENERAL INFORMATION:
; APPLICANT: Billing-Medel, Patricia A.

APPLICANT: Cohen, Maurice
APPLICANT: Colpitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Gordon, Julian
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvill, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Stroupe, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5972.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6183952e
US-08-912-276-16
Query Match 16.7%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 22 EFCPALVSELDPEFF 36
DB 1 EFCPALVSELDPEFF 15
RESULT 10
US-08-912-276-19
Sequence 19, Application US/08912276
Patent No. 6183952
GENERAL INFORMATION:
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colpitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Gordon, Julian
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvill, Jon D.

APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Stroupe, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5972.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6183952e
US-08-912-276-19
Query Match 16.7%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 54 EAVAAKLGVRCTDQ 68
DB 1 EAVAAKLGVRCTDQ 15
RESULT 11
US-08-912-276-17
Sequence 17, Application US/08912276
Patent No. 6183952
GENERAL INFORMATION:
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colpitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Gordon, Julian
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvill, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Stroupe, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories

STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5972.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6183952e
US-08-912-276-17

Query Match 16.7%; Score 15; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 ISEPLFKLSLAKFDA 51
DB 1 ISEPLFKLSLAKFDA 15

RESULT 12
US-08-912-276-18
Sequence 18, Application US/08912276
Patent No. 6183952
GENERAL INFORMATION:
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colpitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Gordon, Julian
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Stroupe, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE BREAST
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5972.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6183952e
US-08-912-276-18

Query Match 16.7%; Score 15; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 SLAKFDAPPEAVNAK 59
DB 1 SLAKFDAPPEAVNAK 15

RESULT 13
US-08-912-276-20
Sequence 20, Application US/08912276
Patent No. 6183952
GENERAL INFORMATION:
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colpitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Gordon, Julian
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Stroupe, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE BREAST
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

* FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5972.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6183952e
US-08-912-276-20

Query Match 16.7%; Score 15; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 MSLOKRSILAEVLK 83
|||||
Db 1 MSLOKRSILAEVLK 15

RESULT 14
US-08-821-451A-2
Sequence 2, Application US/08821451A
Patent No. 6066724
GENERAL INFORMATION:
APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
TITLE OF INVENTION: Human Endometrial Specific Steroid-
TITLE OF INVENTION: Binding Factor I, II and III
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,451A
FILING DATE: March 21, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/014,724
FILING DATE: March 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-821-451A-2

Query Match 8.9%; Score 8; DB 3; Length 90;

Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LALCCYQA 19
|||||
Db 12 LALCCYQA 19

RESULT 15
US-09-263-810-2
Sequence 2, Application US/09263810
Patent No. 6174992
GENERAL INFORMATION:
APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
TITLE OF INVENTION: Human Endometrial Specific Steroid-
TITLE OF INVENTION: Binding Factor I, II and III
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,810
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/821,451
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-263-810-2

Query Match 8.9%; Score 8; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LALCCYQA 19
|||||
Db 12 LALCCYQA 19

Search completed: January 2, 2003, 15:01:30
JOD time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:56:08 : Search time 13 Seconds
(without alignments)
287.144 Million cell updates/sec

Title: US-09-806-301-2
Perfect score: 90
Sequence: 1 MKLSVCLLVTLALCCYQAN.....LQKRSLIAEVLVKKCSV 90

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476320 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	90	1	LPPB_HUMAN
2	8	8.9	91	1	UTER_HUMAN
3	8	8.9	112	1	PSC2_RAT
4	8	8.9	279	1	P87P_RAT
5	7	7.8	90	1	LPPA_HUMAN
6	7	7.8	141	1	HBA_BALAC
7	7	7.8	141	1	HBA_CERSI
8	7	7.8	141	1	HBA_ERIEU
9	7	7.8	141	1	HBA_RHIUN
10	7	7.8	141	1	HBA_TAPTE
11	7	7.8	141	1	HBA_TURTR
12	7	7.8	168	1	YBPQ_BACSU
13	7	7.8	177	1	YGO9_SYNY3
14	7	7.8	248	1	PCRB_METTH
15	7	7.8	328	1	LAID_ECOLI
16	7	7.8	339	1	CWC2_YEAST
17	7	7.8	344	1	STSY_RAUSE
18	7	7.8	352	1	RNPD_ECO57
19	7	7.8	352	1	RNPD_ECOLI
20	7	7.8	424	1	YG5Y_YEAST
21	7	7.8	431	1	NOOE_THETH
22	7	7.8	453	1	NH12_CABEL
23	7	7.8	470	1	SNX_HUMAN
24	7	7.8	683	1	LCEH_HUMAN
25	7	7.8	3079	1	ITR2_HUMAN
26	6	6.7	34	1	ITR2_MOMCO
27	6	6.7	44	1	YCRC_MYCCA
28	6	6.7	73	1	RCRO_BPD3
29	6	6.7	91	1	UTER_LBPCA
30	6	6.7	91	1	UTER_RABIT
31	6	6.7	99	1	NEUY_DICLA
32	6	6.7	112	1	YOXA_BACSU
33	6	6.7	113	1	DHSD_COXBU

34	6	6.7	114	1	YFEC_ECOLI	P27239	escherichia
35	6	6.7	129	1	RECA_BACTN	045791	bacterioides
36	6	6.7	129	1	VDBP_CAMVC	P03552	cauliflower
37	6	6.7	129	1	VDBP_CAMVE	002967	cauliflower
38	6	6.7	129	1	VDBP_CAMVN	000967	cauliflower
39	6	6.7	134	1	YTKC_BACSU	034863	bacillus su
40	6	6.7	140	1	HBA_TRAST	P04237	trachelaphus
41	6	6.7	141	1	HBA_ARCGA	P41329	arctoccephal
42	6	6.7	141	1	HBAI_BOSMU	P01967	bos mutus g
43	6	6.7	141	1	HBAI_BUBBU	091507	bubalus bub
44	6	6.7	141	1	HBAI_GALCR	P14239	galago cras
45	6	6.7	141	1	HBAI_HYLLA	091535	hylobates 1

ALIGNMENTS

RESULT 1	ID	LPBP_HUMAN	STANDARD:	PRT:	90 AA.
AC	095969:				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Lipophilin B precursor (Secretoglobin family 1D member 2).				
GN	SCGB1D2 OR LIPHB.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99167354; PubMed=10066439;				
RA	Zhao C., Nguyen T., Yusifov T., Glasgow H.J., Lehrer R.I.;				
RT	"Lipophilins: human peptides homologous to rat prostatein.";				
RL	Biochem. Biophys. Res. Commun. 256:147-155(1999).				
CC	-1- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND				
CC	ESTRADIOL, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.				
CC	MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.				
CC	-1- SUBCELLULAR LOCATION: Secreted (Potential).				
CC	-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION WAS FOUND IN SKELETAL				
CC	MUSCLE. EXPRESSED AS WELL IN THYMUS, TRACHEA, KIDNEY, STEROID				
CC	RESPONSIVE TISSUES (PROSTATE, TESTIS, UTERUS, BREAST AND OVARY),				
CC	AND SALIVARY GLAND.				
CC	-1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN				
CC	SUBFAMILY.				
CC	-----				
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CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (see http://www.isb.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: AJ224172; GAN1864.1; -				
DR	GeneW: HGNC:18396; SCGB1D2.				
DR	InterPro: IPR000329; Uterogloblin.				
DR	Pfam: PF01099; Uterogloblin; 1.				
DR	PRINTS: PR00486; UTEROGLOBIN.				
DR	SMART: SM00096; UTS; 1.				
KW	Signal.				
FT	SIGNAL 1 21				POTENTIAL.
FT	CHAIN 22 90				LIPOPHILIN B.
SQ	SEQUENCE 90 AA; 9925 MW; 17BB555ED015D1AF CRC64;				
QY	1 MKLSVCLLVTLALCCYQANAEFCPALVSELDLFFTSSEPLFKLSLAKFPAPRAVAKL 60				
DB	1 MKLSVCLLVTLALCCYQANAEFCPALVSELDLFFTSSEPLFKLSLAKFPAPRAVAKL 60				

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OY 61 GVKRCTDQMSLOKRSIAEVLVILKRCV 90
    |||||||||||||||||||||||||||
DB 61 GVKRCTDQMSLOKRSIAEVLVILKRCV 90

RESULT 2
UTER_HUMAN
ID UTER_HUMAN STANDARD: PRT: 91 AA.
AC P1684: Q9UCM4: Q9UCM2:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Clara cell phospholipid-binding protein precursor (CCBP) (Clara cells
DE 10 kDa secretory protein) (CC10) (Uteroglobin) (Urine protein 1)
DE (UPI).
GN SCGB1A1 OR UGB OR CC10 OR CCSP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=89000784; PubMed=3167058;
RA Singh G., Katyal S.L., Brown W.E., Phillips S., Kennedy A.L.,
RA Anthony J., Squeglia N.;
RT "Amino-acid and cDNA nucleotide sequences of human Clara cell 10 kDa
RT protein.";
RL Biochim. Biophys. Acta 950:329-337(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95250987; PubMed=7733299;
RA Hay J.G., Daniel C., Chu C., Crystal R.G.;
RT "Human CC10 gene expression in airway epithelium and subchromosomal
RT locus suggests linkage to airway disease.";
RL Am. J. Physiol. 268:L565-L575(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-18 FROM N.A.
RX MEDLINE=9350776; PubMed=1284526;
RA Wolf M., Klug J., Hackenberg R., Gessler M., Grzeschik K.-H.,
RA Beato M., Suske G.;
RT "Human CC10, the homologue of rabbit uteroglobin: genomic cloning,
RT chromosomal localization and expression in endometrial cell lines.";
RL Hum. Mol. Genet. 1:371-378(1992).
RN [5]
RP SEQUENCE OF 22-74.
RC TISSUE-Urine;
RX MEDLINE=93016476; PubMed=1400743;
RA Okutani R., Itoh Y., Hirata H., Kasahara T., Mukaida N., Kawai T.;
RT "Simple and high-yield purification of urine protein 1 using
RT immunofluorescence chromatography: evidence for the identity of urine
RT protein 1 and human Clara cell 10-kilodalton protein.";
RL J. Chromatogr. A 577:25-35(1992).
RN [6]
RP SEQUENCE OF 22-45.
RC TISSUE-Urine;
RX MEDLINE=93009001; PubMed=1395029;
RA Bernard A., Roels H., Lauwers R., Witters R., Gielens C.,
RA Soumilion A., Van Damme J., De Ley M.;
RT "Human urinary protein 1: evidence for identity with the Clara cell
RT protein and occurrence in respiratory tract and urogenital
RT secretions.";
RL Clin. Chim. Acta 207:239-249(1992).
RN [7]
RP SEQUENCE OF 22-33.
RX MEDLINE=21648993; PubMed=11789998;

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RA Chatouri B., Stahlbom B., Tagesson C., Lindahl M.;
RT "Newly identified proteins in human nasal lavage fluid from
RT non-smokers and smokers using two-dimensional gel electrophoresis and
RT peptide mass fingerprinting.";
RN Proteomics 2:112-120(2002).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95393197; PubMed=7664082;
RA Umland T.C., Swaminathan S., Singh G., Warty V., Furey W.,
RA Pletcher J., Sax M.;
RT "Structure of a human Clara cell phospholipid-binding protein-ligand
RT complex at 1.9-A resolution.";
RN Nat. Struct. Biol. 1:538-545(1994).
CC -1- FUNCTION: BINDS PHOSPHATIDYLCHOLINE, PHOSPHATIDYLINOSITOL,
CC POLYCHLORINATED BIPHENYLS (PCB) AND WEAKLY PROGESTERONE, POTENT
CC INHIBITOR OF PHOSPHOLIPASE A2.
CC -1- SUBUNIT: Homodimer; antiparallel disulfide-linked.
CC -1- TISSUE SPECIFICITY: CLARA CELLS (NONCILIATED CELLS OF THE
CC SURFACE EPITHELIUM OF THE PULMONARY AIRWAYS).
CC -1- SIMILARITY: BELONGS TO THE UTEROGLIBIN FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X13197; CAA31584.1; -
DR EMBL: U01101; AAA1885.1; -
DR EMBL: U01102; AAA18297.1; -
DR EMBL: BC004481; AAH04481.1; -
DR EMBL: X59875; CAA42532.1; -
DR PIR: J50036; JS0036.
DR PIR: S26651; S26651.
DR HSP: P02779; 10TG.
DR Genew: HGNC:12523; SCGB1A1.
DR MIM: 192020; -
DR InterPro: IPR003628; Uteroglbn.sub.
DR InterPro: IPR000329; Uteroglobin.
DR Pfam: PF01099; Uteroglobin.1.
DR PRINTS: PR00486; UTEROGLIBIN.
DR PRODOM: PD012475; Uteroglbn_sub; 1.
DR SMART: SM00096; UTG; 1.
DR PROSITE: PS00403; UTEROGLIBIN_1; 1.
DR PROSITE: PS00404; UTEROGLIBIN_2; 1.
KW Phospholipase A2 inhibitor; Signal; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 91 CLARA CELL PHOSPHOLIPID-BINDING PROTEIN.
FT DISULFID 24 24 INTERCHAIN (WITH C-90').
FT DISULFID 90 90 INTERCHAIN (WITH C-24').
FT VARIANT 56 56 R -> G (IN DBSNP:1802634).
FT VARIANT /FTID-VR_012045.
FT VARIANT 68 68 T -> A (IN DBSNP:1802632).
FT VARIANT /FTID-VR_012046.
FT CONFLICT 24 24 C -> E (IN REF. 7).
FT SEQUENCE 91 AA; 9994 MW; FE65ACA678F12ABD CRC64;
SO Query Match 8.9%; Score 8; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 9 LVTALACC 16
DB 9 LVTALACC 16

RESULT 3
PSC2_RAT
ID PSC2_RAT STANDARD: PRT: 112 AA.
AC P02781;
DT 21-JUL-1986 (Rel. 01, Created)

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DT 01-JAN-1988 (Rel. 06, last sequence update)
 DT 30-MAY-2000 (Rel. 39, last annotation update)
 DE Prostatic steroid-binding protein C2 chain precursor (Prostatein
 peptide C2).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBITaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87146484; PubMed=2881277;
 RA Delaney B., Dirckx L., Decourt J.-L., Claessens F., Peeters B.,
 RA Rombaux W.;
 RT "Rat prostatic binding protein: the complete sequence of the C2 gene
 and its flanking regions";
 RL Nucleic Acids Res. 15:1627-1641(1987).
 RN [2]
 RP SEQUENCE OF 21-112.
 RX MEDLINE=83209619; PubMed=6343081;
 RA Peeters B., Heyns W., Mous J., Rombaux W.;
 RT "Structural studies on rat prostatic binding protein. The primary
 structure of component C2 from subunit S.";
 RL Eur. J. Biochem. 132:669-679(1983).
 RN [3]
 RP SEQUENCE OF 1-100 FROM N.A.
 RX MEDLINE=82220075; PubMed=6896362;
 RA Parker M., Needham M., White R.;
 RT "Prostatic steroid binding protein: gene duplication and steroid
 binding.";
 RL Nature 298:92-94(1982).
 CC -1- FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY
 CC GLYCOPROTEIN OF VENTRAL PROSTATE GLAND.
 CC -1- SUBUNIT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED
 CC C1, C2 AND C3. THESE FORM COVALENT C1:C3 (F) AND C2:C3 (S)
 CC HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC
 CC (C1:C3/C3:C2) PROSTATEIN MOLECULES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: LINKED BY THREE DISULFIDE BONDS TO C3.
 CC -1- MISCELLANEOUS: THE HETERODIMER CAN BIND NON-POLAR STEROIDS,
 CC CHOLESTEROL AND A GROUP OF SMALL PROLINE-RICH PEPTIDES.
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN
 CC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X05034; CAA28708.1; -;
 DR EMBL: V01256; CAA24569.1; -;
 DR EMBL: J00776; AAA51641.1; -;
 DR PIR: A03251; BORT2.
 DR PIR: A26671; A26671.
 DR InterPro: IPR000329; Uteroglobln.
 DR PROSITE: PS00403; UTEROGLOBIN_1; FALSE_NEG.
 DR PROSITE: PS00404; UTEROGLOBIN_2; FALSE_NEG.
 KW Steroid-binding; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 112
 FT MOD_RES 21 112
 FT DISULFID 28 28
 FT DISULFID 69 69
 FT DISULFID 92 92
 FT CONFLICT 26 26
 FT CONFLICT 88 88
 FT CONFLICT 96 112
 FT SEQUENCE 112 AA; 12828 MW; DA65A6A82E677864 CRC64;
 Query Match 8.9%; Score 8; DB 1; Length 112;

Best Local Similarity 100.0%; Pred. No. 0.57;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 49 FDPAPPEAV 56
 ID SPBP_RAT STANDARD; PRT; 279 iA.
 AC P08723;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Prostatic spermine-binding protein precursor (SBP).
 GN SBP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBITaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87137538; PubMed=3818623;
 RA Chang C., Saltzman A.G., Hlipakka R.A., Huang I.-Y., Liao S.;
 RT "Prostatic spermine-binding protein. Cloning and nucleotide sequence
 of cDNA, amino acid sequence, and androgenic control of mRNA level.";
 RL J. Biol. Chem. 262:2826-2831(1987).
 RN [2]
 RP SEQUENCE, AND REVISIONS.
 RX MEDLINE=89000602; PubMed=3166977;
 RA Anderegg R.J., Carr S.A., Huang I.-Y., Hlipakka R.A., Chang C.,
 RA Liao S.;
 RT "Correction of the cDNA-derived protein sequence of prostatic
 RT spermine binding protein: pivotal role of tandem mass spectrometry in
 RT sequence analysis.";
 RL Biochemistry 27:4214-4221(1988).
 CC -1- FUNCTION: SPERMINE-BINDING PROTEIN IS AN ANDROGEN REGULATED
 CC VENTRAL PROSTATE GLYCOPROTEIN THAT BINDS VARIOUS POLYAMINES.
 CC -1- TISSUE SPECIFICITY: PROSTATE.
 CC -1- SIMILARITY: TO MOUSE SBP.
 CC -----
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 CC -----
 DR EMBL: J02675; AAA2113.1; ALT_SEQ.
 DR PIR: A29561; A29561.
 DR PIR: A28714; A28714.
 DR InterPro: IPR001229; Jacalin_lectin.
 DR Pfam: PF01419; Jacalin; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 279
 FT MOD_RES 18 18
 FT CARBOHYD 62 62
 FT DOMAIN 154 279
 FT SEQUENCE 279 AA; 31080 MW; 3BBE01A02517A65 CRC64;
 Query Match 8.9%; Score 8; D3 1; Length 279;
 Best Local Similarity 100.0%; Pred. No. 1.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 LLVLTAL 14
 ID 2 LLVLTAL 9
 RESULT 5

```

LPPA_HUMAN
ID LPPA_HUMAN STANDARD: PRT; 90 AA.
AC 095968;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lipophilin A precursor (Secretoglobin family 1D member 1).
GN SCGB1D1 OR LIPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99167354; PubMed=10066439;
RA Zhao C., Nguyen T., Yusifov T., Glasgow B.J., Lehrer R.I.;
RA "Lipophilins: human peptides homologous to rat prostatein.";
RL Biochem. Biophys. Res. Commun. 256:147-155(1999).
RN [2]
RP SEQUENCE OF 22-90, AND MASS SPECTROMETRY.
RX MEDLINE=98385871; PubMed=9720917;
RA Lehrer R.I., Xu G., Abduragimov A., Dinh N.N., Qu X.-D., Martin D.,
RA Glasgow B.J.;
RA "Lipophilin, a novel heterodimeric protein of human tears.";
RL FEBS Lett. 432:163-167(1998).
CC -1- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS. MAY ALSO BIND
CC ESTRADIOL, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.
CC MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.
CC -1- SUBUNIT: HETERODIMER OF A LIPOPHILIN A AND A LIPOPHILIN C
CC (MAMMALOBLIN B) MONOMER ASSOCIATED HEAD TO HEAD.
CC -1- SUBCELLULAR LOCATION: Secreted (potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LACRIMAL GLAND, THYMUS, KIDNEY,
CC TESTIS, OVARY AND SALIVARY GLAND.
CC -1- MASS SPECTROMETRY: MW=7574.69; METHOD=Electrospray; RANGE=22-90.
CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN
CC SUBFAMILY.
CC -----
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CC -----
CC EMBL: AJ224171; CA11863.1; -.
CC DR Genew; HGNC:18395; SCGB1D1.
CC DR InterPro: IPR000329; uteroglobln.
CC DR Pfam: PF01099; Uteroglobln; 1.
CC DR PRINTS: PR00486; UTEROGLOBIN.
CC DR SMART: SM00096; UTG; 1.
CC KW Signal.
CC FT CHAIN 1 21 LIPOPHILIN A.
CC FT SIGNAL 1 21
CC FT CHAIN 22 90
CC SQ SEQUENCE 90 AA; 9898 MW; DE2DAF7565A87D34 CRC64;

Query Match 7.8%; Score 7; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LSVCLL 9
DB 3 LSVCLL 9

RESULT 6
HBA_BALAC STANDARD: PRT; 141 AA.
AC P18971;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobin alpha chain.

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GN HBA.
OS Balenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balenopteridae; Balenoptera.
OX NCBI_Taxid=9767;
RN [1]
RP SEQUENCE.
RA Abbas A., Rucknagel P., Matsuda G., Zaidi Z.H., Brannitser G.;
RA "The primary structure of Minke-whale (Balenoptera acutorostrata -
RA Cetacea) hemoglobin.";
RT J. Chem. Soc. Pak. 6:253-256(1984).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: Heterotrimer of two alpha chains and two beta chains.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC PIR: S06520; HAHMK.
CC HSSP: P01922; 1B20.
CC InterPro: IPR002338; Alpha_haem.
CC DR InterPro: IPR000971; Globin.
CC Pfam: PF00042; globin; 1.
CC DR PRINTS: PR00612; ALPHAHAEM.
CC DR PROSITE: PS01033; GLOBIN; 1.
CC KW Heme; Oxygen transport; Transport; Erythrocyte;
CC Polymorphism.
CC FT METAL 58 58 IRON (HEME DISTAL LIGAND).
CC FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
CC FT VARIANT 21 21 G -> S.
CC FT VARIANT 96 96 A -> V.
CC SQ SEQUENCE 141 AA; 15406 MW; 0B0C26CDF7B72B53 CRC64;

Query Match 7.8%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVTTLAL 14
DB 105 LVTTLAL 111

RESULT 7
HBA_CERST STANDARD: PRT; 141 AA.
AC P01963;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobin alpha chain.
GN HBA.
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI_Taxid=9807;
RN [1]
RP SEQUENCE.
RX MEDLINE=83055102; PubMed=7141412;
RA Mazur G., Brannitser G., Wright P.G.;
RA "The primary structure of the hemoglobin from a white rhinoceros
RA (Ceratotherium simum, perissodactyla): beta 2 Glu.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1077-1085(1982).
CC -1- FUNCTION: Involved in oxygen transport from the lung to the
CC various peripheral tissues.
CC -1- SUBUNIT: Heterotrimer of two alpha chains and two beta chains.
CC -1- TISSUE SPECIFICITY: Red blood cells.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
CC PIR: A02286; HARNW.
CC HSSP: P01958; 2MBH.
CC InterPro: IPR002338; Alpha_haem.
CC DR InterPro: IPR000971; Globin.
CC Pfam: PF00042; globin; 1.
CC DR PRINTS: PR00612; ALPHAHAEM.
CC DR PROSITE: PS01033; GLOBIN; 1.

```

KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 58 IRON (HEME DISTAL LIGAND).
 SO SEQUENCE 141 AA; 15303 MW; 8BDC6A7B8DE0DB9 CRC64;
 Query Match 7.8%; Score 7; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVTAL 14
 |||||
 Db 105 LVTAL 111

RESULT 8
 HBA_ERIEU STANDARD; PRT; 141 AA.
 ID HBA_ERIEU
 AC P01949;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hemoglobin alpha chain.
 GN HBA.
 OS Erythraeus europaeus (Western European hedgehog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
 OX NCBI_TaxID=9365;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79109529; PubMed=762046;
 RA Maita T., Araya A., Matsuda G., Goodman M.;
 RT "Amino acid sequences of the alpha and beta chains of adult
 hemoglobin of the European hedgehog, Erythraeus europaeus.";
 RL J. Biochem. 85:259-268(1979).
 CC -1- FUNCTION: Involved in oxygen transport from the lung to the
 CC various peripheral tissues.
 CC -1- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.
 CC -1- TISSUE SPECIFICITY: Red blood cells.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A02271; HAH.
 DR HSSP: P01922; IBZ0.
 DR InterPro: IPR002338; Alpha_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00612; ALPHAAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 58 IRON (HEME DISTAL LIGAND).
 FT METAL 87 IRON (HEME PROXIMAL LIGAND).
 SO SEQUENCE 141 AA; 15122 MW; E4EE4DE6485050F6 CRC64;
 Query Match 7.8%; Score 7; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVTAL 14
 |||||
 Db 105 LVTAL 111

RESULT 9
 HBA_RH1UN STANDARD; PRT; 141 AA.
 ID HBA_RH1UN
 AC P09906;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hemoglobin alpha chain.
 GN HBA.
 OS Rhinoceros unicornis (Greater Indian rhinoceros).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Rhinoceros.
 OX NCBI_TaxID=9809;

RN [1]
 RP SEQUENCE.
 RX MEDLINE=87271129; PubMed=3606819;
 RA Abdast A., Weber R.E., Braunitzer G., Gollenboth R.;
 RT "Molecular basis for ATP/2,3-bisphosphoglycerate control switch-over
 (poikilotherm/homeotherm) an intermediate amino-acid sequence in the
 RT hemoglobin of the great Indian rhinoceros (Rhinoceros unicornis,
 RT Perissodactyla).";
 RL Biol. Chem. Hoppe-Seyler 368:323-332(1987).
 CC -1- FUNCTION: Involved in oxygen transport from the lung to the
 CC various peripheral tissues.
 CC -1- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.
 CC -1- TISSUE SPECIFICITY: Red blood cells.
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
 DR PIR: A26543; A26543.
 DR HSSP: P01958; IIBE.
 DR InterPro: IPR002338; Alpha_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00612; ALPHAAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte.
 FT METAL 58 IRON (HEME DISTAL LIGAND).
 FT METAL 87 IRON (HEME PROXIMAL LIGAND).
 SO SEQUENCE 141 AA; 15319 MW; 9612DA629640B260 CRC64;
 Query Match 7.8%; Score 7; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 7.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVTAL 14
 |||||
 Db 105 LVTAL 111

RESULT 10
 HBA_TAPTE STANDARD; PRT; 141 AA.
 ID HBA_TAPTE
 AC P01962;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hemoglobin alpha-1 and alpha-2 chains.
 OS Tapirus terrestris (Lowland tapir) (Brazilian tapir).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
 OX NCBI_TaxID=9801;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85053021; PubMed=6149994;
 RA Mazur G., Braunitzer G.;
 RT "Perissodactyla: the primary structure of hemoglobins from the
 RT lowland tapir (Tapirus terrestris): glutamic acid in position 2 of
 RT the beta chains.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:1057-1106(1984).
 CC -1- FUNCTION: Involved in oxygen transport from the lung to the
 CC various peripheral tissues.
 CC -1- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.
 CC -1- TISSUE SPECIFICITY: Red blood cells.
 CC -1- POLYMORPHISM: THERE ARE TWO ALLELES. THE SEQUENCE SHOWN IS THAT OF
 CC ALPHA-1.
 DR PIR: A02285; HATPI.
 DR PIR: A91727; HATP2.
 DR HSSP: P01958; 2MB.
 DR InterPro: IPR002338; Alpha_haem.
 DR InterPro: IPR000971; Globin.
 DR Pfam: PF00042; globin; 1.
 DR PRINTS: PR00612; ALPHAAEM.
 DR PROSITE: PS01033; GLOBIN; 1.
 KW Heme; Oxygen transport; Transport; Erythrocyte;
 KW Polymorphism.
 FT METAL 58 58 IRON (HEME DISTAL LIGAND).

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FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
FT VARIANT 115 115 D -> G (IN ALPHA-2).
SQ SEQUENCE 141 AA; 15290 MW; E3727EB650C5BD1 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LVTTLAL 14
RN 11111111
DB 105 LVTTLAL 111

RESULT 11
HBA_TURTR STANDARD; PRT; 141 AA.
ID HBA_TURTR
AC P18978;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Hemoglobin alpha chain.
HBA.
OS Turlops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Turlops.
OX NCBI_TaxID=9739;
RN 11
RP SEQUENCE.
RX MEDLINE=84052510; PubMed=6639644;
RA Klineschmidt T., Braunitzer G.;
RT "The primary structure of hemoglobins from the bottlenosed dolphin
(RT) (Turlops truncatus, Cetacea).";
RL Biomed. Biochim. Acta 42:685-695(1983).
CC -1- FUNCTION: Involved in oxygen transport from the lung to the
CC various peripheral tissues.
CC -1- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.
CC -1- TISSUE SPECIFICITY: Red blood cells.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR HSP: S06522; HADD.
DR HSP: P01922; IBZ0.
DR Interpro: IPR002338; Alpha_haem.
DR Interpro: IPR000971; Globin.
DR Pfam: PF00042; globin.1.
DR PRINTS: PR00612; ALPHAHAEM.
DR PROSITE: PS01033; GLOBIN.1.
KW Heme; Oxygen transport; Transport; Erythrocyte.
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
SQ SEQUENCE 141 AA; 15344 MW; 6F449EF5920E3F2C CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LVTTLAL 14
RN 11111111
DB 105 LVTTLAL 111

RESULT 12
YBPQ_BACSU STANDARD; PRT; 168 AA.
ID YBPQ_BACSU
AC P54158;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein ypbQ.
YBPQ.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN 11

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RP SEQUENCE FROM N.A.
RC STRAIN=168 / Marburg;
RX MEDLINE=96349105; PubMed=8760912;
RA Sorokin A.V., Azevedo V., Zumbstein E., Galleron N., Ehrlich S.D.,
RA Serror P.;
RT "Sequence analysis of the Bacillus subtilis chromosome region between
RT the serA and kdg loci cloned in a yeast artificial chromosome.";
RL Microbiology 142:2005-2016(1996).
[12]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessières P., Bolyen A., Borcherdt S.,
RA Borries R., Bourster L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Ertlan K.D., Erington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haelegh J., Harwood C.R., Henaut A.,
RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Jois B., Karamata D., Kasahara Y., Klaerr-Bianchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogilwa A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portelle D., Porwoll S., Prescott A.M.,
RA Prescan E., Puig C., Purnelle B., Rapoport G., Ray M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeder R., Scofield F.,
RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Yamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambuit R., Wedler E., Wedler H., Wetzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yaman K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zumbstein A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
[13]
RP SEQUENCE OF 155-168 FROM N.A.
RX MEDLINE=93374837; PubMed=8396117;
RA Chen L., James L.P., Hellmann J.D.;
RT "Metalloregulation in Bacillus subtilis: isolation and
RT characterization of two genes differentially repressed by metal
RT ions.";
RL J. Bacteriol. 175:5428-5437(1993).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL, L77246; AAA96614.1; -.
DR EMBL, Z99115; CAB14121.1; -.
DR EMBL, L19548; -; NOT ANNOTATED_CDS.
DR EMBL, Z22929; -; NOT ANNOTATED_CDS.
DR Subtilisin; Bg11603; ypbQ.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 1 21 POTENTIAL.
FT TRANSMEM 41 61 POTENTIAL.
FT TRANSMEM 68 88 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.
SQ SEQUENCE 168 AA; 19316 MW; 23F1B604F08F8E55 CRC64;

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Query Match          7.8%; Score 7; DB 1; Length 168;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 SLIAEVL 81
Db 53 SLIAEVL 59

RESULT 13
YG09_SYNY3 STANDARD; PRT; 177 AA.
AC P73844;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein sll1609.
GN SLL1609.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Natsu K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- SIMILARITY: TO SYNECHOCYSTIS PCC 6803 SLA1290 AND SLL0925.
CC -----
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CC or send an email to license@isb-sib.ch).
CC DR EMBL: D90910; BAA17903.1;
CC KW Hypothetical protein: Complete proteome.
CC SQ SEQUENCE 177 AA; 20457 MW; F4B40D935AFD2138 CRC64;

Query Match          7.8%; Score 7; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 SLIAEVL 81
Db 106 SLIAEVL 112

RESULT 14
PCRB_METTH STANDARD; PRT; 248 AA.
AC 026652;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE PCRB protein homolog.
GN PCRB OR MTH552.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Delta H;
RT MEDLINE=98037514; PubMed=9371463;

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RA Smith D.R., Doucette-Stamm L.A., Delonghney C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson S.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-T., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- SIMILARITY: BELONGS TO THE PCRB FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC CC -----
CC DR EMBL: AE000838; AAB85058.1;
CC DR InterPro: IPR003009; FMN_enzyme.
CC DR InterPro: IPR002911; PCRB.
CC DR Pfam: PF01884; PCRB; 1.
CC DR TIGRPFAMs: TIGR00265; PCRB; 1.
CC KW Complete proteome.
CC SQ SEQUENCE 248 AA; 26525 MW; F59DAE240731E662 CRC64;

Query Match          7.8%; Score 7; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 VKRCTDQ 68
Db 191 VKRCTDQ 197

RESULT 15
LAI1_ECOLI STANDARD; PRT; 328 AA.
AC P76316; 008478; 008479;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative l-aminocyclopropane-1-carboxylate deaminase (EC 4.1.99.4)
DE (ACC deaminase).
GN YED0 OR B1919.
GN YED0 OR B1919.
OS Escherichia coli.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
CC -----
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RX STRAIN=K12;
CC RX MEDLINE=97251358; PubMed=9097040;
CC RA Itoh T., Alpa H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
CC RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
CC RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
CC RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
CC RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
CC RA Yamamoto Y., Horiuchi T.;
CC RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
CC corresponding to the 40.1-50.0 min region on the linkage map.";

```

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RL DNA Res. 3:379-392(1996).
CC -1- CATALYTIC ACTIVITY: 1-aminocyclopropane-1-carboxylate + H(2)O - 2-
CC Oxobutanate + NH(3).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACC DEAMINASE FAMILY.
CC -----
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CC -----
CC EMBL; AE000284; AAC74986.1; ALT_INIT.
DR EMBL; D90832; BAA15739.1; ALT_INIT.
DR EMBL; D90833; BAA15746.1; ALT_INIT.
DR EcoGene; EG14038; yedO.
DR InterPro; IPR001926; B6_enzyme_beta.
DR Pfam; PF00291; PALP; 1.
DR TIGRFAMs; TIGR01275; ACC_deam_rel; 1.
KW Hypothetical protein; Lyase; Pyridoxal phosphate; Complete proteome.
FT BINDING 51 51 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 328 AA; 35133 MW; 4179DE645C0B32D8 CRC64;

Query Match 7.8%; Score 7; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AVAAKLG 61
DB 86 AVAAKLG 92

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Search completed: January 2, 2003, 15:00:10
 Job time : 14 secs

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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:58:33 ; Search time 29 Seconds
(without alignments)
639.457 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 90

Sequence: 1 MKLSVCLLVTLALCCYQAN.....LQKRSLIAEVLVKIKKCSV 90

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	8.9	70	12 Q91FH2	Q91fh2 chilo. iride
2	8	8.9	90	6 Q9GK65	Q9gk65 oryctolagus
3	8	8.9	217	8 Q37435	Q37435 cepaea nemo
4	8	8.9	255	16 Q9ZOU8	Q9zou8 rhizobium m
5	8	8.9	335	10 Q65330	Q65330 elaeagnus u
6	8	8.9	688	16 Q9HYU9	Q9hyu9 pseudomonas
7	7	7.8	90	6 Q9GK67	Q9gk67 oryctolagus
8	7	7.8	96	6 Q8WMS2	Q8wms2 oryctolagus
9	7	7.8	102	6 Q9BH17	Q9bh17 globodera p
10	7	7.8	107	5 Q95Q19	Q95q19 caenorhabdi
11	7	7.8	111	11 Q91XL7	Q91xl7 speromphili
12	7	7.8	123	5 P91445	P91445 caenorhabdi
13	7	7.8	132	16 Q9EX03	Q9ex03 streptomyce
14	7	7.8	133	16 Q965Y1	Q965y1 rhizobium l
15	7	7.8	139	17 Q8ZTL9	Q8ztl9 pyrobaculum
16	7	7.8	160	8 Q8WAH0	Q8wah0 hadra belle

17	7	7.8	160	8 Q8WAG9	Q8wag9 hadra belle
18	7	7.8	160	8 Q8WAG8	Q8wag8 hadra belle
19	7	7.8	160	8 Q8WAG7	Q8wag7 hadra belle
20	7	7.8	160	8 Q8WAG6	Q8wag6 hadra belle
21	7	7.8	160	8 Q8WAG5	Q8wag5 hadra belle
22	7	7.8	160	8 Q8WAG4	Q8wag4 hadra belle
23	7	7.8	160	8 Q8WAG3	Q8wag3 hadra belle
24	7	7.8	160	8 Q8WAG2	Q8wag2 hadra belle
25	7	7.8	160	8 Q8WAG1	Q8wag1 spherospir
26	7	7.8	160	8 Q8WAG0	Q8wag0 spherospir
27	7	7.8	160	8 Q8WAF9	Q8waf9 spherospir
28	7	7.8	160	8 Q8WAF8	Q8waf8 spherospir
29	7	7.8	160	8 Q8WAF7	Q8waf7 spherospir
30	7	7.8	160	8 Q8W8S3	Q8w8s3 hadra belle
31	7	7.8	160	8 Q8W8P6	Q8w8p6 hadra belle
32	7	7.8	160	8 Q8W8P5	Q8w8p5 hadra belle
33	7	7.8	160	8 Q8W8P0	Q8w8p0 hadra belle
34	7	7.8	160	8 Q8W8L1	Q8w8l1 hadra belle
35	7	7.8	160	8 Q8W8Z4	Q8w8z4 hadra belle
36	7	7.8	160	8 Q8W8Z3	Q8w8z3 hadra belle
37	7	7.8	160	8 Q8W7D5	Q8w7d5 hadra belle
38	7	7.8	160	8 Q8W7D4	Q8w7d4 hadra belle
39	7	7.8	161	8 Q9MTD3	Q9mtd3 bombycilla
40	7	7.8	165	16 Q9ZRA5	Q9zra5 rhizobium m
41	7	7.8	166	16 Q9HWF2	Q9hwf2 pseudomonas
42	7	7.8	170	10 Q9MBH0	Q9mbh0 arabidopsis
43	7	7.8	173	15 Q41766	Q41766 human t-lym
44	7	7.8	187	17 Q8ZX32	Q8zx32 pyrobaculum
45	7	7.8	189	10 Q40064	Q40064 hordeum vul

ALIGNMENTS

RESULT 1
Q91FH2 PRELIMINARY; PRT; 70 AA.
AC Q91FH2
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 352R.
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
OX NCBI_TaxID=10488;
RN [1]
RP SEQUENCE FROM N.A.
RA Delius H., Darai G., Fluegel R.M.;
RT "DNA analysis of insect iridescent virus 6: evidence for circular
RT permutation and terminal redundancy.";
RL J. Virol. 49:609-614(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86174607; PubMed=3959991;
RA Lorbacher de Ruiz H., Gelderblom H., Hofmann W., Darai G.;
RT "Insect iridescent virus type 6 induced toxic degenerative hepatitis
RT in mice.";
RL Med. Microbiol. Immunol. 175:43-53(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87321126; PubMed=2820141;
RA Scholtzler P., Soltan J.B., Fischer M., Reiser H., Scholz J.,
RA Delius H., Darai G.;
RT "Molecular cloning and physical mapping of the genome of insect
RT iridescent virus type 6: further evidence for circular permutation of
RL the viral genome.";
RN Virology 160:66-74(1987).
RP SEQUENCE FROM N.A.
RX MEDLINE=89073752; PubMed=3201750;
RA Fischer M., Scholtzler P., Delius H., Darai G.;
RT "Identification and characterization of the repetitive DNA element in
RT the genome of insect iridescent virus type 6.";

RL Virology 167:485-496(1998).
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92196996; PubMed-1549908;
 RA Handermann M., Schmitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,
 RA Darai G.;
 RT "Identification and mapping of origins of DNA replication within the
 RT DNA sequences of the genome of insect iridescent virus type 6.";
 RL Virus Genes 6:19-32(1992).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93118242; PubMed-1475907;
 RA Sonntag K.C., Darai G.;
 RT "Characterization of the third origin of DNA replication of the genome
 RT of insect iridescent virus type 6.";
 RL Virus Genes 6:333-342(1992).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93260401; PubMed-8492091;
 RA Stomwasser R., Raab K., Schmitzler P., Janssen W., Darai G.;
 RT "Identification of the gene encoding the major capsid protein of
 RT insect iridescent virus type 6 by polymerase chain reaction.";
 RL J. Gen. Virol. 74:873-879(1993).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94167241; PubMed-8121799;
 RA Schmitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,
 RA Delius H., Darai G.;
 RT "Identification of genes encoding zinc finger proteins, non-histone
 RT chromosomal HMG protein homologue, and a putative GTP phosphohydrolase
 RT in the genome of Chilo iridescent virus.";
 RL Nucleic Acids Res. 22:158-166(1994).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94353641; PubMed-8073636;
 RA Sonntag K.C., Schmitzler P., Koonin E.V., Darai G.;
 RT "Chilo iridescent virus encodes a putative helicase belonging to a
 RT distinct family within the DEAD/H superfamily: implications for the
 RT evolution of large DNA viruses.";
 RL Virus Genes 8:151-158(1994).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95213160; PubMed-7698884;
 RA Sonntag K.C., Schmitzler P., Janssen W., Darai G.;
 RT "Identification of the primary structure and the coding capacity of
 RT the genome of insect iridescent virus type 6 between the genome
 RT coordinates 0.310 and 0.347 (7990 bp).";
 RL Intervirology 37:287-297(1994).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-94292906; PubMed-8021587;
 RA Schmitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,
 RA Koonin E.V., Darai G.;
 RT "Insect iridescent virus type 6 encodes a polypeptide related to the
 RT largest subunit of eukaryotic RNA polymerase II.";
 RL J. Gen. Virol. 75:1557-1567(1994).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98141693; PubMed-9482589;
 RA Bahr U., Tidona C.A., Darai G.;
 RT "The DNA sequence of Chilo iridescent virus between the genome
 RT coordinates 0.101 and 0.391: similarities in coding strategy between
 RT insect and vertebrate Iridoviruses.";
 RL Virus Genes 15:235-245(1997).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99125223; PubMed-9926400;
 RA Muller K., Tidona C.A., Bahr U., Darai G.;
 RT "Identification of a thymidylate synthase gene within the genome of
 RT Chilo iridescent virus.";
 RL Virus Genes 17:243-258(1998).
 RN
 RP SEQUENCE FROM N.A.

RX MEDLINE-99383793; PubMed-10456793;
 RA Muller K., Tidona C.A., Darai G.;
 RT "Identification of a gene cluster within the genome of Chilo
 RT iridescent virus encoding enzymes involved in viral DNA replication
 RT and processing.";
 RL Virus Genes 18:243-264(1999).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21342589; PubMed-11448171;
 RA Jakob N.J., Muller K., Bahr U., Darai G.;
 RT "Analysis of the First Complete DNA Sequence of an Invertebrate
 RT Iridovirus: Coding Strategy of the Genome of Chilo Iridescent Virus.";
 RL Virology 286:182-196(2001).
 RN
 RP SEQUENCE FROM N.A.
 RA Jakob N.J., Muller K., Bahr U., Darai G.;
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF303741; AAK82213.1;
 SQ SEQUENCE 70 AA; 8112 MW; 0098F56C3EB39A42 CRC64;

 Query Match 8.9%; Score 8; DB 12; Length 70;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 80 VLVKILKK 87
 DB 58 VLVKILKK 65

 RESULT 2
 Q9GK65 PRELIMINARY; PRT; 90 AA.
 AC Q9GK65;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Lipophilin BL.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LACRIMAL GLAND;
 RA Zhao C., Nguyen T.X., Lehrer R.I.;
 RT "Rabbit Lipophilins.";
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF308616; AAG42804.1;
 DR InterPro: IPR000329; Uteroglobin.
 DR Pfam: PF01099; Uteroglobin; 1.
 DR PRINTS: PR00486; UTEROGLBIN.
 SQ SEQUENCE 90 AA; 9943 MW; 410900DF7F3EB1BC CRC64;

 Query Match 8.9%; Score 8; DB 6; Length 90;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 10 VTALACY 17
 DB 10 VTALACY 17

 RESULT 3
 Q37435 PRELIMINARY; PRT; 217 AA.
 AC Q37435;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cytochrome oxidase subunit II.
 OS Cepaea nemoralis (banded wood snail).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;

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OC Helicaceae; Helicidae; Cepaea.
OX NCBI_TaxID=28835;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEPATOPANCREAS;
RX MEDLINE=97077301; PubMed=8919868;
RA Terrett J.A., Miles S., Thomas R.H.;
RT "Complete DNA sequence of the mitochondrial genome of Cepaea nemoralis
  (Gastropoda: Pulmonata).";
RT J. Mol. Evol. 42:160-168(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=HEPATOPANCREAS;
RX MEDLINE=97207848; PubMed=9055084;
RA Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
  Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
  Watanabe K., Thomas R.H.;
RT "Evolution of pulmonate gastropod mitochondrial genomes: comparisons
  of complete gene organizations of Euhadra, Cepaea and Albinaria and
  implications of unusual tRNA secondary structures.";
RT Genetics 145:749-758(1997).
RL EMBL: U23045; AAC09520.1; -.
DR InterPro: IPR001505; Copper_CuA.
DR InterPro: IPR002429; Cyt_c-ox_2.
DR InterPro: IPR002088; PPTA.
DR InterPro: IPR000822; Znf_C2H2.
DR Pfam: PF02790; COX2_TM; 1.
DR ProDom: PD000131; Copper_CuA; 1.
DR PROSITE: PS00904; PPTA; UNKNOWN_1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW Mitochondrion.
SQ SEQUENCE 217 AA; 25135 MW; 98DA7B7E0E3DC14 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 8; Length 217;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLLVLTAL 14
  |||||
Db 71 LLLVLTAL 78

RESULT 4
0920J8 PRELIMINARY; PRT; 255 AA.
AC 0920J8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative outer membrane protein.
GN R01322 OR SMC01342.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gonzy J., Bothe G., Ampe F., Batut J.,
  Boissard P., Becker A., Boutry M., Cadieu E., Dreno S., Gloux S.,
  Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
  Pohl T., Portetelle D., Puhler A., Purnelle B., Ransperger U.,
  Renard C., Thebaud P., Vandenberg M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
  Sinorhizobium meliloti strain 1021.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL: AL591786; CAC45901.1; -.
DR InterPro: IPR000063; Thiorod.
DR PROSITE: PS00194; THIOREDOXIN; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 255 AA; 27353 MW; 302E0EA668861EE1 CRC64;

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Query Match
Best Local Similarity 100.0%; Score 8; DB 16; Length 255;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AVAAKLG 62
  |||||
Db 181 AVAAKLG 188

RESULT 5
065330 PRELIMINARY; PRT; 335 AA.
AC 065330;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Acidic chitinase (EC 3.2.1.14).
OS Eleagnus umbellata (Autumn olive).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Rosales; Elaeagnaceae; Elaeagnus.
OX NCBI_TaxID=43233;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ROOT NODULE;
RA Kim H.-B., An C.-S.;
RT "Isolation and characterization of cDNA clone encoding acidic
  chitinase from the root nodule of Eleagnus umbellata.";
RT Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF061805; AAC16010.1; -.
DR HSSP: P23951; 2BA.
DR InterPro: IPR001002; Chitin_binding_1.
DR InterPro: IPR00726; Glyco_hydro_19.
DR Pfam: PF00187; Chitin_bind_1; 1.
DR Pfam: PF00182; Glyco_hydro_19; 1.
DR PRINTS: PR00451; CHITINBINDNG.
DR ProDom: PD000574; Glyco_hydro_19; 1.
DR SMART: SM00270; ChnBD; 1.
DR PROSITE: PS00773; CHITINASE_19_1; 1.
DR PROSITE: PS00774; CHITINASE_19_2; 1.
DR PROSITE: PS00026; CHITIN_BINDING; 1.
KW Chitin binding; Glycosidase; Hydrolase.
SQ SEQUENCE 335 AA; 35737 MW; ICC09BB877A18E0 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 10; Length 335;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VCLLVLT 12
  |||||
Db 9 VCLLVLT 16

RESULT 6
09HYU9 PRELIMINARY; PRT; 686 AA.
AC 09HYU9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Hypothetical protein PA3294.
GN PA3294.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
  Hickey M.J., Brinkman F.S.L., Hufnagle V.O., Kowalik D.J., Lagrou M.,

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RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Iarbig K., Lam R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reiter J., Satter M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an
 opportunistic pathogen.";
 RL Nature 406:959-964 (2000).
 DR EMBL: AE004751; AAC06682.1; -;
 KM Hypothetical protein; Complete proteome.
 SQ SEQUENCE 688 AA; 77042 MW; 844ED9E9BA6D64 CRC64;

Query Match 8.9%; Score 8; DB 16; Length 688;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 APPENAVAA 58
 |||||||
 DB 655 APPENAVAA 662

RESULT 7

O9GK67 PRELIMINARY; PRT; 90 AA.
 AC O9GK67:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Lipophilin AL.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LACRIMAL GLAND;
 RA Zhao C., Nguyen T.X., Lehrer R.I.;
 RT "Rabbit Lipophilins.";
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF308614; AAG42802.1; -;
 DR InterPro: IPR000329; Uteroglobulin.
 DR Pfam: PF01099; Uteroglobulin; 1.
 DR SMART: SM00096; UTG; 1.
 SQ SEQUENCE 90 AA; 9762 MW; 6D34F9540C1FF742 CRC64;

Query Match 7.8%; Score 7; DB 6; Length 90;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 DAPPEAV 56
 |||||||
 DB 50 DAPPEAV 56

RESULT 8

O8WMS2 PRELIMINARY; PRT; 96 AA.
 AC O8WMS2:
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Lipophilin AL2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LACRIMAL GLAND;
 RA Lind-Ayres M.R., Crow J.M., Steelman C.A., Nelson J.D.,
 RA Remington S.G.;
 RT "Lipophilin AL2 of the male rabbit lacrimal gland.";
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY063770; AAL40859.1; -;

DR InterPro: IPR000329; Uterogloblin.
 DR Pfam: PF01099; Uterogloblin; 1.
 SQ SEQUENCE 96 AA; 10510 MW; 48EC2972D0EA78C4 CRC64;

Query Match 7.8%; Score 7; DB 6; Length 96;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 TLALCCY 17
 |||||||
 DB 11 TLALCCY 17

RESULT 9

O9BH17 PRELIMINARY; PRT; 102 AA.
 AC O9BH17:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE FMRFamide-related peptide 2 (Fragment).
 GN Flp-2.
 OS Globodera pallida.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
 OC Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
 OX NCBI_TaxID=36090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA 2/3;
 RX MEDLINE=21414099; PubMed=11522352;
 RA Kimber M.J., Fleming C.C., Bjourson A.J., Halton D.W., Maule A.G.;
 RT "FMRFamide-related peptides in potato cyst nematodes.";
 RL MOL. Biochem. Parasitol. 116:199-208 (2001).
 DR EMBL: AJ300488; CAC32452.1; -;
 FT CHAIN 89 >98 FMRFAMIDE-RELATED PEPTIDE 2.
 FT NON_TER 102 102
 SQ SEQUENCE 102 AA; 11609 MW; A0BB68EB0891A484 CRC64;

Query Match 7.8%; Score 7; DB 5; Length 102;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LLLVTLA 13
 |||||||
 DB 9 LLLVTLA 15

RESULT 10

O95Q19 PRELIMINARY; PRT; 107 AA.
 AC O95Q19:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Y51H4A.26 protein.
 GN Y51H4A.26.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sulston J.E.;
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C. elegans*: A platform for
 investigating biology.";
 RL Science 282:2012-2018 (1998).
 DR EMBL: AL132952; CAC70119.1; -;
 SQ SEQUENCE 107 AA; 12323 MW; 766B3FC05D9C14E0 CRC64;


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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed-11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Matsumoto A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DK EMBL; AP003011; BAB3572.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 133 AA; 14765 MW; 7E8FD06159E231A CRC64;

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Query Match          7.8%; Score 7; DB 16; Length 133;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 51 APPEAVA 57
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DB 99 APPEAVA 105

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RESULT 15

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O82TL9          PRELIMINARY;      PRT;    139 AA.
AC O82TL9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Possible heat shock protein, hspX homolog part 1, authentic
DE frameshift.
GN PAE3193A.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed-11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum."
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DK EMBL; AE009916; AAL64741.1; -.
KW Heat shock; Complete proteome.
SQ SEQUENCE 139 AA; 14562 MW; 96BE53856A3BE60F CRC64;

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Query Match          7.8%; Score 7; DB 17; Length 139;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 55 AVAAKLG 61
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DB 77 AVAAKLG 83

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Search completed: January 2, 2003, 15:00:46
 Job time : 31 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2003, 14:53:27 ; Search time 14 Seconds
(without alignments)
189.147 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 450
Sequence: 1 MKLSVCLLVTLALCCYQAN.....LQKRLIAEVLVLEKSCV 90

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfilst1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	450	100.0	90	3	US-08-821-451A-4	Sequence 4, App1
2	450	100.0	90	4	US-09-263-810-4	Sequence 4, App1
3	450	100.0	90	4	US-08-912-276-15	Sequence 15, App1
4	450	100.0	90	4	US-09-583-169-4	Sequence 4, App1
5	450	100.0	90	4	US-09-215-818-6	Sequence 6, App1
6	342	76.0	69	4	US-08-812-276-23	Sequence 23, App1
7	277	61.6	90	3	US-08-821-451A-2	Sequence 2, App1
8	277	61.6	90	4	US-09-263-810-2	Sequence 2, App1
9	277	61.6	90	4	US-09-583-169-2	Sequence 2, App1
10	219	48.7	45	4	US-08-912-276-22	Sequence 22, App1
11	202	44.9	90	3	US-08-821-451A-25	Sequence 25, App1
12	202	44.9	90	3	US-08-821-451A-26	Sequence 26, App1
13	202	44.9	90	4	US-09-263-810-25	Sequence 25, App1
14	202	44.9	90	4	US-09-263-810-26	Sequence 26, App1
15	202	44.9	90	4	US-09-583-169-25	Sequence 25, App1
16	202	44.9	90	4	US-09-583-169-26	Sequence 26, App1
17	110	24.4	91	1	US-08-455-896-8	Sequence 8, App1
18	110	24.4	91	2	US-08-933-149-8	Sequence 8, App1
19	110	24.4	91	2	US-09-082-343-8	Sequence 8, App1
20	110	24.4	91	3	US-09-082-353-8	Sequence 8, App1
21	110	24.4	91	5	PCT-US96-08235-8	Sequence 8, App1
22	101	22.4	22	4	US-08-912-276-21	Sequence 21, App1
23	80	17.8	15	4	US-08-912-276-16	Sequence 16, App1
24	75.5	16.7	15	2	US-08-964-725-14	Sequence 14, App1
25	75	16.7	15	4	US-08-912-276-19	Sequence 19, App1
26	73	16.2	16	4	US-08-912-276-18	Sequence 18, App1
27	72	16.0	16	4	US-08-912-276-17	Sequence 17, App1

28	70	15.6	109	1	US-07-662-193-5	Sequence 5, App1
29	70	15.6	109	3	US-08-300-928C-8	Sequence 8, App1
30	70	15.6	109	3	US-08-430-944F-8	Sequence 8, App1
31	70	15.6	109	3	US-08-430-014-8	Sequence 8, App1
32	70	15.6	109	3	US-08-431-184-8	Sequence 8, App1
33	69	15.3	1621	4	US-08-972-927-3	Sequence 3, App1
34	66.5	14.8	224	4	US-08-287-959-6	Sequence 6, App1
35	66.5	14.8	3079	5	PCT-US94-0019F-4	Sequence 4, App1
36	66	14.7	16	4	US-08-912-276-20	Sequence 20, App1
37	62	13.8	109	1	US-07-807-529J-6	Sequence 6, App1
38	62	13.8	109	5	PCT-US93-0246J-6	Sequence 6, App1
39	62	13.8	111	1	US-07-662-193-4	Sequence 4, App1
40	62	13.8	111	3	US-08-300-928C-6	Sequence 6, App1
41	62	13.8	111	3	US-08-430-944I-6	Sequence 6, App1
42	62	13.8	111	3	US-08-430-014-6	Sequence 6, App1
43	62	13.8	111	3	US-08-431-184-6	Sequence 6, App1
44	62	13.8	145	2	US-08-832-535-2	Sequence 2, App1
45	62	13.8	145	3	US-09-019-485-2	Sequence 2, App1

ALIGNMENTS

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RESULT 1
US-08-821-451A-4
; Sequence 4, Application US/08821451A
; Patent No. 6066724
;
GENERAL INFORMATION:
; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; TITLE OF INVENTION: Binding Factor I, II and III
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821,451A
; FILING DATE: March 21, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,724
; FILING DATE: March 21, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
;
INFORMATION FOR SEO ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
;
US-08-821-451A-4
;
Query Match 100.0%; Score 450, DB 3; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MKLSVCLLVLTALCCYQANAEECPALVSELDFFFIISPLFKLSIAKFDAPPEAVAAKL 60
QY 61 GVKRCTDQMSLOKRSILAEVLVKILKCSV 90
Db 61 GVKRCTDQMSLOKRSILAEVLVKILKCSV 90

RESULT 2
US-09-263-810-4

; Sequence 4, Application US/09263810
; Patent No. 6174992
; GENERAL INFORMATION:
; APPLICANT: Jian NI, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; TITLE OF INVENTION: Binding Factor I, II and III
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,810
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/821,451
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-09-263-810-4
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Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKLSVCLLVLTALCCYQANAEECPALVSELDFFFIISPLFKLSIAKFDAPPEAVAAKL 60

QY 61 GVKRCTDQMSLOKRSILAEVLVKILKCSV 90
Db 61 GVKRCTDQMSLOKRSILAEVLVKILKCSV 90

RESULT 3
US-08-912-276-15

; Sequence 15, Application US/08912276
; Patent No. 6183952
; GENERAL INFORMATION:
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice

; APPLICANT: Colpitts, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Gordon, Julian
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klass, Michael R.
; APPLICANT: Kratochvil, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Russell, John C.
; APPLICANT: Strome, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,276
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5972.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TEXEL:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6183952e

US-08-912-276-15

Query Match 100.0%; Score 450; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKLSVCLLVLTALCCYQANAEECPALVSELDFFFIISPLFKLSIAKFDAPPEAVAAKL 60

QY 61 GVKRCTDQMSLOKRSILAEVLVKILKCSV 90
Db 61 GVKRCTDQMSLOKRSILAEVLVKILKCSV 90

RESULT 4
US-09-583-169-4

; Sequence 4, Application US/09583169
; Patent No. 6338948
; GENERAL INFORMATION:
; APPLICANT: Jian NI, Guo-Liang Yu and Reiner Gentz
; TITLE OF INVENTION: Human Endometrial Specific Steroid-
; TITLE OF INVENTION: Binding Factor I, II and III
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/583,169
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/821,451
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-583-169-4

Query Match 100.0%; Score 450; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFPAPPAVAKL 60
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DB 61 GVKRCTDQMSIQKRSLLAEVLVYKILKKCV 90

RESULT 5
US-09-215-818-6
Sequence 6, Application US/09215818A
Patent No. 6379671
GENERAL INFORMATION:
APPLICANT: Colpitts, Tracey
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
FILE REFERENCE: 5972-US-P2
CURRENT APPLICATION NUMBER: US/09/215,818A
EARLIER FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/912,276
EARLIER FILING DATE: 1997-08-17
EARLIER APPLICATION NUMBER: 08/697,105
EARLIER FILING DATE: 1996-08-19
EARLIER APPLICATION NUMBER: 08/912,149
EARLIER FILING DATE: 1997-08-15
EARLIER APPLICATION NUMBER: 08/697,106
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 90
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-215-818-6

Query Match 100.0%; Score 450; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFPAPPAVAKL 60
DB 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFPAPPAVAKL 60
QY 61 GVKRCTDQMSIQKRSLLAEVLVYKILKKCV 90
DB 61 GVKRCTDQMSIQKRSLLAEVLVYKILKKCV 90

RESULT 6
US-08-912-276-23
Sequence 23, Application US/08912276
Patent No. 6183952
GENERAL INFORMATION:
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colpitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Gordon, Julian
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kralovich, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Stroupe, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE BREAST
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5972-US-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6183952e
US-08-912-276-23

Query Match 76.0%; Score 342; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 8e-36;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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Db      1 MRSLSTLAWSLALCTCYOHALVCPVAASELIVLFISDAANVLDQAKLNPPEALAAKL 60
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QY      61 GVKRCTDMSLQKRSLLAEVLVILKKCSV 90
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1 CLASSIFICATION:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER:
4 FILING DATE:
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Becker, Cheryl L
7 REGISTRATION NUMBER: 35,441
8 REFERENCE/DOCKET NUMBER: 5972.US.PI
9 TELECOMMUNICATION INFORMATION:
10 TELEPHONE: 847/935-1729
11 TELEFAX: 847/938-2623
12
13 INFORMATION FOR SEQ ID NO: 22:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 45 amino acids
16 TYPE: amino acid
17 STRANDEDNESS: single
18 TOPOLOGY: linear
19 MOLECULE TYPE: No. 618395ze
20 US-08-912-276-22
21
22 Query Match 48.7%; Score 219; DB 4; Length 45;
23 Best Local Similarity 100.0%; Prid. No. 1.2e-20;
24 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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26 Oy 46 LAKFAPPEAVAAKLGVRCTDOMSLQKRSLIAEYVILTKCSV 90
27 ||||||||||||||||||||||||||||||||||||||||||||
28 Db 1 LAKFAPPEAVAAKLGVRCTDOMSLQKRSLIAEYVILTKCSV 45
29
30 RESULT 11
31 US-08-821-451A-25
32 Sequence 25, Application US/08821451A
33 Patent No. 6066724
34
35 GENERAL INFORMATION:
36 APPLICANT: Jian NI, Guo-Liang Yu and Reiner Gentz
37 TITLE OF INVENTION: Human Endometrial Specific Steroid-
38 TITLE OF INVENTION: Binding Factor I, II and III
39 NUMBER OF SEQUENCES: 27
40 CORRESPONDENCE ADDRESS:
41 ADDRESSEE: CARELLA, BYRNE, BAIN, GILLILAN,
42 ADDRESSEE: CECCHI, STEWART & OLSTEIN
43 STREET: 6 BECKER FARM ROAD
44 CITY: ROSELAND
45 STATE: NEW JERSEY
46 COUNTRY: USA
47 ZIP: 07068
48
49 COMPUTER READABLE FORM:
50 MEDIUM TYPE: 3.5 INCH DISKETTE
51 COMPUTER: IBM PS/2
52 OPERATING SYSTEM: MS-DOS
53 SOFTWARE: WORD PERFECT 5.1
54 CURRENT APPLICATION DATA:
55 APPLICATION NUMBER: US/08/821,451A
56 FILING DATE: March 21, 1997
57 CLASSIFICATION: 435
58 PRIOR APPLICATION DATA:
59 APPLICATION NUMBER: 60/014,724
60 FILING DATE: March 21, 1996
61 ATTORNEY/AGENT INFORMATION:
62 NAME: MULLINS, J.G.
63 REGISTRATION NUMBER: 33,073
64 REFERENCE/DOCKET NUMBER: 325800-521 (P257)
65 TELECOMMUNICATION INFORMATION:
66 TELEPHONE: 201-994-1700
67 TELEFAX: 201-994-1744
68 INFORMATION FOR SEQ ID NO: 25:
69 SEQUENCE CHARACTERISTICS:
70 LENGTH: 90 AMINO ACIDS
71 TYPE: AMINO ACID
72 STRANDEDNESS: SINGLE
73 TOPOLOGY: LINEAR
74 MOLECULE TYPE: PROTEIN

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 2, 2003, 15:00:53 : Search time 11 seconds
(without alignments)
155.058 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 90

Sequence: 1 MKLSVCLLVLTALCYQAN.....LQKSLIAEVLKILKCSV 90

Scoring table:

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Searched: 117078 seqs, 18951520 residues

Word size : 0

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	90	US-09-825-301-77	Sequence 77, Appl
2	90	100.0	90	US-09-110-716-29	Sequence 29, Appl
3	90	100.0	90	US-09-934-054-1	Sequence 1, Appl
4	90	100.0	90	US-09-985-911-4	Sequence 4, Appl
5	69	76.7	69	US-09-110-716-37	Sequence 37, Appl
6	50	55.6	50	US-09-864-761-44240	Sequence 44240, A
7	8	8.9	74	US-09-110-716-38	Sequence 38, Appl
8	8	8.9	83	US-09-992-598-260	Sequence 260, App
9	8	8.9	83	US-09-989-293A-260	Sequence 260, App
10	8	8.9	83	US-09-989-735-260	Sequence 260, App
11	8	8.9	83	US-09-990-444-260	Sequence 260, App
12	8	8.9	83	US-09-989-730-260	Sequence 260, App
13	8	8.9	83	US-09-990-436-260	Sequence 260, App
14	8	8.9	83	US-09-991-181-260	Sequence 260, App
15	8	8.9	83	US-09-993-687-260	Sequence 260, App
16	8	8.9	83	US-09-989-722-260	Sequence 260, App
17	8	8.9	83	US-09-989-723-260	Sequence 260, App
18	8	8.9	83	US-09-989-279-260	Sequence 260, App
19	8	8.9	83	US-09-989-727-260	Sequence 260, App

20	8	8.9	83	US-09-989-721-260	Sequence 260, App
21	8	8.9	83	US-09-989-732-260	Sequence 260, App
22	8	8.9	83	US-09-991-073-260	Sequence 260, App
23	8	8.9	83	US-09-990-442-260	Sequence 260, App
24	8	8.9	83	US-09-991-163-260	Sequence 260, App
25	8	8.9	83	US-09-993-604-260	Sequence 260, App
26	8	8.9	83	US-09-990-456-260	Sequence 260, App
27	8	8.9	83	US-09-989-721-260	Sequence 260, App
28	8	8.9	90	US-09-985-911-2	Sequence 2, Appl
29	8	8.9	112	US-09-934-034-8	Sequence 8, Appl
30	8	7.8	90	US-09-110-716-27	Sequence 27, Appl
31	7	7.8	166	US-09-815-242-5162	Sequence 5162, App
32	7	7.8	223	US-10-052-586-210	Sequence 210, App
33	7	7.8	288	US-09-925-297-617	Sequence 617, App
34	7	7.8	352	US-09-912-02C-293	Sequence 293, App
35	7	7.8	570	US-08-825-486-2	Sequence 2, Appl
36	7	7.8	570	US-08-870-434-7	Sequence 7, Appl
37	7	7.8	570	US-09-372-044-2	Sequence 2, Appl
38	7	7.8	648	US-09-923-831-43	Sequence 43, Appl
39	7	7.8	739	US-09-974-298-159	Sequence 159, App
40	7	7.8	762	US-09-925-299-998	Sequence 998, App
41	6	6.7	36	US-10-120-319-18	Sequence 18, Appl
42	6	6.7	36	US-09-733-524-11	Sequence 11, Appl
43	6	6.7	43	US-09-864-761-39434	Sequence 39434, A
44	6	6.7	43	US-09-864-761-41268	Sequence 41268, A
45	6	6.7	45	US-09-864-761-36472	Sequence 36472, A

ALIGNMENTS

RESULT 1
US-09-825-301-77
; Sequence 77, Application US/09825301
; Patent No. US20020009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiaqun
; APPLICANT: Zehentner, Barbara
; TITLE OF INVENTION: PERSING, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 77
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-825-301-77

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Best Local Similarity 100.0% Pred. No. 1.8e-81:
Matches 90: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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DB 1 MKLSVCLLVLTALCYQANAEPCPALVSELDFFITSEPLFKSLAKFDAPPEAAVAKL 60

QY 61 GYKRCIDQMSLOKRSIAEVLKILKCSV 90
DB 61 GYKRCIDQMSLOKRSIAEVLKILKCSV 90

RESULT 2
US-09-110-716-29
; Sequence 29, Application US/09110716A
; Patent No. US20020034739A1
; GENERAL INFORMATION:

APPLICANT: Lehrer, Robert I.
APPLICANT: Zhao, Chengquan
TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
FILE REFERENCE: 22000-20596.00
CURRENT APPLICATION NUMBER: US/09/110.716A
CURRENT FILING DATE: 1998-07-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 90
TYPE: PRT
ORGANISM: lipophilin B
US-09-110-716-29

Query Match
Query Similarity 100.0%; Score 90; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.8e-81;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFIISPLFKLSLAKFDAPPEAVAAKL 60

QY 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90
DB 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90

RESULT 3
US-09-934-054-1
Sequence 1, Application US/09934054
Patent No. US20020107385A1
GENERAL INFORMATION:
APPLICANT: Akerblom, Ingrid E.
Hillman, Jennifer L.
Murry, Lynn E.
Goli, Surya K.
Hawkins, Phillip R.
TITLE OF INVENTION: BREAST TUMOR SPECIFIC PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025-6936
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/934.054
FILING DATE: 21-Aug-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/747.547
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PR-0077 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-934-054-1

Query Match
Query Similarity 100.0%; Score 90; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.8e-81;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFIISPLFKLSLAKFDAPPEAVAAKL 60

QY 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90
DB 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90

RESULT 4
US-09-985-911-4
Sequence 4, Application US/09985911
Patent No. US20020151012A1
GENERAL INFORMATION:
APPLICANT: NI ET AL.
TITLE OF INVENTION: HUMAN ENDOMETRIAL SPECIFIC STEROID-BINDING FACTOR I, II AND II
FILE REFERENCE: PF257D3
CURRENT APPLICATION NUMBER: US/09/985.911
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 09/583,169
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 09/263,810
PRIOR FILING DATE: 1999-03-08
PRIOR APPLICATION NUMBER: 08/821,451
PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION NUMBER: 60/014,724
PRIOR FILING DATE: 1996-03-21
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 90
TYPE: PRT
ORGANISM: human
US-09-985-911-4

Query Match
Query Similarity 100.0%; Score 90; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.8e-81;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFIISPLFKLSLAKFDAPPEAVAAKL 60

QY 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90
DB 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90

RESULT 5
US-09-110-716-37
Sequence 37, Application US/09110716A
Patent No. US20020034739A1
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Zhao, Chengquan
TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
FILE REFERENCE: 22000-20596.00
CURRENT APPLICATION NUMBER: US/09/110.716A
CURRENT FILING DATE: 1998-07-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37
LENGTH: 69
TYPE: PRT
ORGANISM: Lpnb
US-09-110-716-37

Query Match 76.7%: Score 69; DB 10; Length 69;
 Best Local Similarity 100.0%: Pred. No. 9.9e-61;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 EFCBALVSELDFFFISEPLEFKLSLAKFDAPPEAVAAKLGKCRCTDMSLQKRSLLAEVL 60

QY 82 VKILKCSV 90
 DB 61 VKILKCSV 69

RESULT 6
 US-09-864-761-44240
 ; Sequence 44240, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aecomica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
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 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
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 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
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 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
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 ; SEQ ID NO 44240
 ; LENGTH: 50
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC004127.1
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
 ; OTHER INFORMATION: EST_HUMAN HIT: AW103293.1, EVALUATE 5.00e-21
 ; OTHER INFORMATION: SWISSPROT HIT: O95969, IVALUE 4.00e-22
 US-09-864-761-44240

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 Best Local Similarity 100.0%: Pred. No. 2.7e-42;
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 DB 1 LDFFIISPLEFKLSLAKFDAPPEAVAAKLGKCRCTDMSLQKRSLLAEVL 50

RESULT 7
 US-09-110-716-38
 ; Sequence 38, Application US/09110716A
 ; Patent No. US20020034739A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehner, Robert I.
 ; APPLICANT: Zhao, Chengquan
 ; APPLICANT: Glasgow, Benjamin J.
 ; TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
 ; FILE REFERENCE: 22000-20596.00
 ; CURRENT APPLICATION NUMBER: US/09/110,716A
 ; CURRENT FILING DATE: 1998-07-07
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 38
 ; LENGTH: 74
 ; TYPE: PRT
 ; ORGANISM: PRC2
 US-09-110-716-38

Query Match 8.9%: Score 8; DB 10; Length 74;
 Best Local Similarity 100.0%: Pred. No. 0.43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 FDAPPEAV 56
 DB 28 FDAPPEAV 35

RESULT 8
 US-09-992-598-260
 ; Sequence 260, Application US/09992598
 ; Patent No. US20020160384A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferreira, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-24
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;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 8.9% Score 8: DB 9: Length 83:
Best Local Similarity 100.0%: Pred.No. 0.4%:
Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 12 LALCCYQA 19
DB 12 LALCCYQA 19

RESULT 9
US-09-989-293A-260
; Sequence 260, Application US/09889293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Getter, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC66
; CURRENT APPLICATION NUMBER: US/09/989,293A

;; CURRENT FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12
;; PRIOR APPLICATION NUMBER: 60/065311
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;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
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;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/087106
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;; PRIOR APPLICATION NUMBER: 60/089105
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;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 8.9%; Score 8; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LALCCYOA 19
Db 12 LALCCYOA 19

RESULT 10
US-09-989-735-260
;; Sequence 260, Application US/09989735
;; Publication No. US20020193299A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnovers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C61
;; CURRENT APPLICATION NUMBER: US/09/989,735
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
;; PRIOR FILING DATE: 1997-11-12

[illegible]

;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 8.9%; Score 8; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LALCCYQA 19
|||
DB 12 LALCCYQA 19

RESULT 11
US-09-990-444-260
; Sequence 260, Application US/09990444
; Publication No. US20020193300A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990.444
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910

;; PRIOR FILING DATE: 1998-03-20
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;; PRIOR FILING DATE: 1998-05-07
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;; PRIOR FILING DATE: 1998-06-16
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;; PRIOR APPLICATION NUMBER: 60/089599
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;; PRIOR FILING DATE: 1998-06-17
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 8.9%; Score 8; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 0 48;
Matches 8; Conservative 0; Mismatched 0; Indels 0; Gaps 0;

QY 12 LALCYOA 19
DB 12 LALCYOA 19

RESULT 12
US-09-989-730-260
;; Sequence 260, Application US/09989730
;; Publication No. US20020197674A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerltsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kjaavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; TITLE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730PIC69
;; CURRENT APPLICATION NUMBER: US/09/989,730
;; CURRENT FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/090696
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PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01	PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-02	PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07	PRIOR APPLICATION NUMBER: 60/091982

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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      8.9%  Score 8;  DB 9;  Length 83;
Best Local Similarity 100.0%, Fred. No. 0.48;
Matches      8;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Oy      12 LALCCYQA 19
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Db      12 LALCCYQA 19

RESULT 13
US-09-990-436-260
; Sequence 260, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC14
; CURRENT APPLICATION NUMBER: US/09/990,436
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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; PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1998-06-19
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PRIOR APPLICATION NUMBER: 60/089948
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 8.9% Score 8: DB 9: Length 83;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LALCCYCA 19
Db 12 LALCCYCA 19

RESULT 14
US-09-991-181-260
Sequence 260, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C53
CURRENT FILING DATE: 2001-11-16
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 8.9%; Score 8; LB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LALCCYQA 19
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Db 12 LALCCYQA 19

RESULT 15
US-09-993-687-260

Sequence 260, Application US/09993687
Publication No. US20020198149A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730pic11
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/090435
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090444
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
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;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090540
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;; PRIOR APPLICATION NUMBER: 60/090542
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090676
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090678
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;; PRIOR APPLICATION NUMBER: 60/090690
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090694
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090862
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 8.9%; Score 8; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

OY 12 LALCCYQA 19
| | | | | | | |
DB 12 LALCCYQA 19

Search completed: January 2, 2003, 15:04:37
Job time : 12 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:52:12 ; Search time 35 Seconds

(without alignments)
342.644 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 450
Sequence: 1 MKLSVCILLVTLALCCYQAN.....LQKSLINEVLKIKKCSV 90

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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2: /SIDS2/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	450	100.0	90	18 AAW35803	Human endometrial
2	450	100.0	90	19 AAW59776	Amino acid sequence
3	450	100.0	90	19 AAW54271	BU101 antigenic pe
4	450	100.0	90	20 AAW89613	Endometrial steroid
5	450	100.0	90	21 AAB13787	Human BU101. Homo
6	450	100.0	90	21 AAB07501	Amino acid sequence
7	450	100.0	90	21 AAB03768	Human endometrial
8	450	100.0	90	21 AAY84875	A human endometria
9	450	100.0	90	22 AAG65989	Lipophilin B polyp
10	450	100.0	90	22 AAE07518	Human Lipophilin B

11	450	100.0	90	22 AAB31681	An endometrial spe
12	450	100.0	90	23 ABB09634	Human endometrial
13	450	100.0	117	22 ABB11907	Human breast tumou
14	450	100.0	120	20 AAY48606	Human breast tumou
15	447	99.3	90	22 AAE07521	Human Lipophilin B
16	445	98.9	90	22 AAE07525	Human Lipophilin B
17	440	97.8	90	22 AAE07524	Human Lipophilin B
18	436	96.9	90	22 AAE07522	Human Lipophilin B
19	435	96.7	90	22 AAE07526	Human Lipophilin B
20	434.5	96.6	89	23 AAO20554	Protein of human L
21	433	96.2	90	22 AAE07527	Human Lipophilin B
22	417	92.7	88	22 AAE07523	Human Lipophilin B
23	342	76.0	69	19 AAW54279	BU101 antigenic pe
24	342	76.0	69	21 AAB07509	Amino acid sequenc
25	277	61.6	90	18 AAW35802	Human endometrial
26	277	61.6	90	21 AAB03767	Human endometrial
27	277	61.6	90	22 AAB31680	An endometrial spe
28	277	61.6	90	23 ABB09633	Human endometrial
29	267	59.3	53	21 AAG00474	Human secreted pro
30	267	59.3	53	21 AAY64680	Human 5' EST relat
31	267	59.3	90	22 AAM23955	Human EST encoded
32	261	58.0	90	23 AAO20553	Human EST encoded
33	254	56.4	102	22 AAB87666	Protein of human L
34	246	54.7	50	22 ABB40007	Bovine mammary tis
35	246	54.7	50	22 AAM60754	Peptide #7513 enco
36	246	54.7	50	22 AAM73426	Human brain expres
37	246	54.7	50	22 AAM73426	Human bone marrow
38	246	54.7	50	22 AAM33628	Peptide #7665 enco
39	244	54.2	79	20 AAY59999	Human peptide enco
40	242	53.8	92	22 AAG26041	Novel human diagno
41	238	52.9	83	21 AAB24417	Human PRO812 prote
42	238	52.9	83	21 AAY66704	Membrane-bound pro
43	238	52.9	83	22 AAU12391	Human PRO812 polyp
44	238	52.9	83	22 AAB65227	Human PRO812 (UNQ5
45	238	52.9	83	19 AAW54278	BU101 antigenic pe

ALIGNMENT:

RESULT 1	AAW35803	AAW35803 standard; Protein; 90 AA.
ID	XX	
AC	AAW35803;	
XX		
DT	27-MAR-1998 (first entry)	
XX		
DE	Human endometrial specific steroid-binding factor II.	
XX		
KW	Endometrial specific steroid-binding factor II; ESF II; human;	
KW	Clara cell secretory protein; endometrial;	
KW	phospholipase A2 inhibitor; polychlorinated biphenyl; antiaggregant;	
KW	inflammation; asthma; rhinitis; cystic fibrosis; airway disease;	
KW	neoplasia; atopy; therapy; diagnosis.	
OS	Homo sapiens.	
XX		
FX	Key	Location/Qualifiers
FT	Peptide	1..21
FT		/label= Sig_peptide
FT	Protein	22..90
FT		/label= Mat_protein
XX		
PN	WO9734997-A1.	
XX		
PD	25-SEP-1997.	
XX		
PF	21-MAR-1996;	96WO-US03857.
XX		
PR	21-MAR-1996;	96WO-US03857.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	

XX Gentz RL, Ni J, Yu G;
 PI
 DR WPI: 1997-480206/44.
 DR N-PSDB: AAT94831.
 XX
 PT Human endometrial specific steroid-binding factor I, II and III -
 PT used to treat inflammation, asthma, rhinitis, cystic fibrosis,
 PT airway disease, neoplasia, atopy etc.
 PS
 PS Claim 18; Page 63-64; 92pp; English.
 XX
 CC This sequence comprises human endometrial specific steroid binding
 CC factor II (ESF II), a protein that inhibits phospholipase A2
 CC activity, binds to polychlorinated biphenyl compounds, reduces
 CC foreign protein antigenicity, inhibits monocyte and neutrophil
 CC chemotaxis and phagocytosis, inhibits platelet aggregation,
 CC regulates eicosanoid levels in the human uterus and controls the
 CC growth of endometrial cells. The amino acid sequence was deduced
 CC from a cDNA clone (see AAT94831) derived from cycloheximide-treated
 CC CEM cells. ESF I (see AAW35802) and ESF III (see AAW35804) are also
 CC claimed. Human ESF II has about 49% identity with rat prostatic
 CC steroid-binding protein. Recombinant ESF I, II and III can be
 CC expressed in host cells for use in claimed methods (a) for treating
 CC a patient in need of ESF I, II or III (including expression of the
 CC polypeptide in vivo) and (b) for identifying compounds which bind
 CC to and inhibit activation of the ESF polypeptide. hESF I, II and
 CC III may be used to treat inflammation, asthma, rhinitis, cystic
 CC fibrosis, airway disease, neoplasia and atopy.
 CC
 XX Sequence 90 AA:
 SO
 Query Match 100.0%; Score 450; DB 18; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEVAAKL 60
 Db 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEVAAKL 60
 Oy 61 GVKRCTDMSLOKRSLLAEVLVKILKCSV 90
 Db 61 GVKRCTDMSLOKRSLLAEVLVKILKCSV 90
 RESULT 2
 ID AAW59776 standard; Protein: 90 AA.
 AC AAW59776;
 XX
 DT 12-OCT-1998 (first entry)
 XX
 DE Amino acid sequence of the human steroid binding protein C1.
 XX
 KW Human steroid-binding protein C1; hSBP1, hSBP2; breast cancer; probe;
 KW gene therapy vector; ribozyme; probe; hybridisation; amplification;
 KW antibody; immunoassay.
 XX
 OS Homo sapiens.
 XX
 PN WO9821331-A1.
 PD 22-MAY-1998.
 XX
 PE 07-NOV-1997; 97WO-US20674.
 XX
 PR 12-NOV-1996; 96US-0747547.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Akerblom IE, Goli SK, Hawkins PR, Hillman JL, Murry LE;
 XX

DR WPI: 1998-297935/26.
 DR N-PSDB: AAV41579.
 XX
 PT New human steroid binding proteins C1 and C2 - useful for, e.g.
 PT diagnosis, monitoring and treating breast cancer, and for drug
 PT screening
 PS
 PS Claim 1; Fig 1; 70pp; English.
 XX
 CC This is the amino acid sequence of the human steroid-binding protein
 CC C1 (hSBP1) used in the method of the invention for the diagnosis,
 CC monitoring and treatment of breast cancer. hSBP1 and hSBP2 are useful
 CC as markers for breast cancer, i.e. measuring levels of hSBP1 and hSBP2
 CC used for diagnosis or monitoring the disease, to identify subjects
 CC at risk and to discriminate between different forms of cancer for
 CC selection of appropriate therapies. They may also be used for drug
 CC screening. Nucleic acids encoding hSBP1 and hSBP2 can be used in gene
 CC therapy vectors to overexpress the steroid-binding proteins, preventing
 CC binding of steroids, or antisense sequences, ribozymes. Their nucleic
 CC acids can also be used for the diagnosis and monitoring (by quantifying
 CC expression of hSBP), as source of probes for hybridisation and
 CC amplification of genomic or related sequences for studying regulation of
 CC gene function and for mapping the genomic sequence. Antibodies are used
 CC as diagnostic reagents in standard immunoassays for hSBP.
 CC
 XX Sequence 90 AA:
 SO
 Query Match 100.0%; Score 450; DB 19; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEVAAKL 60
 Db 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEVAAKL 60
 Oy 61 GVKRCTDMSLOKRSLLAEVLVKILKCSV 90
 Db 61 GVKRCTDMSLOKRSLLAEVLVKILKCSV 90
 RESULT 3
 ID AAW54271 standard; Protein: 90 AA.
 AC AAW54271;
 XX
 DT 29-JUL-1998 (first entry)
 XX
 DE BUI01 antigenic peptide epitope 1.
 XX
 KW BUI01; breast cancer; diagnosis; prevention; treatment; gene therapy;
 KW immunisation; drug screening; epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO9807857-A1.
 PD 26-FEB-1998.
 XX
 PE 19-AUG-1997; 97WO-US14665.
 XX
 PR 15-AUG-1997; 97US-0912276.
 PR 19-AUG-1996; 96US-0697105.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;
 PI Gordon J, Granadosen, Hodges SC, Klass MR, Kratochvil JD;
 PI Roberts-rapp L, Russell JC, Stroupe SD;
 XX
 DR WPI: 1998-169161/15.
 DR N-PSDB: AAV26461.
 XX

PT New BU101 protein over-expressed in breast cancer - useful for, e.g.
 PT diagnosis, treatment and prevention of breast cancer
 XX
 PS Claim 17; Page 90; 105pp; English.
 XX
 CC This represents a BU101 polypeptide sequence. BU101 is a member of the
 CC uteroglobin family of proteins and is over-expressed in breast cancer.
 CC Cells transformed with a recombinant expression system comprising a
 CC sequence derived from the BU101 open reading frame and with at least 50
 CC percent identity to the sequences shown in AAY26458 to AAY26461 are used
 CC to produce BU101 polypeptides containing at least 1 epitope. These are
 CC used to detect BU101-specific antibodies which are used correspondingly
 CC to detect BU101 antigens. The BU101 polynucleotide sequences can be used
 CC in a method for detecting the presence of a target BU101 polynucleotide.
 CC The various assays are used for diagnosis, prognosis, staging,
 CC monitoring, treating and preventing diseases of the breast (especially
 CC cancer and its metastases), and also for determining susceptibility. The
 CC BU101 polypeptides are also useful in drug screening, e.g. to identify
 CC antagonists of BU101, potentially useful therapeutically and as targets
 CC for therapy. The antibodies are also useful for targeted drug delivery
 CC and therapeutically to neutralise BU101 polypeptides. Fragments of the
 CC BU101 nucleic acid are useful as probes and primers, e.g. for detection
 CC of altered gene expression or in fluorescent in situ hybridisation, also
 CC in gene therapy to generate antisense or ribozyme molecules or for
 CC genetic immunisation.
 CC
 XX
 SQ Sequence 90 AA;
 Query Match 100.0%; Score 450; DB 19; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFITSEPLFKSLAKFDAPPVAAKL 60
 DB 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFITSEPLFKSLAKFDAPPVAAKL 60
 QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
 RESULT 4
 AAM89613
 ID AAM89613; standard; Protein; 90 AA.
 AC AAM89613;
 XX
 DT 25-MAR-1999 (first entry)
 XX
 DE Endometrial steroid binding protein II.
 XX
 KW Endometrial steroid binding protein II; ESBPII; cancer; detection;
 KW endometriosiis; endometrial fibroid; mammary cancer.
 XX
 OS Homo sapiens.
 XX
 PN MO9856248-A1.
 XX
 PD 17-DEC-1998.
 XX
 PF 09-JUN-1998; 98WO-US12053.
 XX
 PR 09-JUN-1997; 97US-0049015.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Schmidt CJ, Wang X;
 XX
 DR WPI: 1999-080843/07.
 DR N-PSDB; AAX00069.
 XX
 PT Treatment of endometrial cancer, mammary cancer, endometriosiis or
 PT endometrial fibroids - comprises administering endometrial steroid

PT binding protein II antagonist
 XX
 PS Disclosure; Page 13; 19pp; English.
 XX
 CC A method has been developed for the treatment of endometrial cancer,
 CC mammary cancer, endometriosiis or endometrial fibroids. The method
 CC comprises administering endometrial steroid binding protein II (ESBPII)
 CC antagonist. Also described in the present invention are: (1) a method
 CC for diagnosing the above mentioned diseases comprising analysing the
 CC abnormally high level of ESBPII polypeptide in cells, tissues and bodily
 CC fluids; and (2) a diagnostic method for the diseases described above
 CC comprising analysing the abnormally high or low transcription level of
 CC ESBPII in cells, tissues and bodily fluids. The methods can be used to
 CC diagnose, treat, and monitor the progression, remission or recurrence of
 CC abnormal cell growth, such as cancers, especially endometrial and
 CC mammary cancer, and endometriosiis and endometrial fibroids. The present
 CC sequence represents ESBPII, from the present invention.
 CC
 XX
 SQ Sequence 90 AA;
 Query Match 100.0%; Score 450; DB 20; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFITSEPLFKSLAKFDAPPVAAKL 60
 DB 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFITSEPLFKSLAKFDAPPVAAKL 60
 QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
 RESULT 5
 AAB13787
 ID AAB13787 standard; Protein; 90 AA.
 AC AAB13787;
 XX
 DT 20-JUN-2001 (first entry)
 XX
 DE Human BU101.
 XX
 KW Human; breast cancer; breast disease detection; mammagloblin;
 KW uteroglobin; BU101; endometrial; cytosatic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 53 /label= Leu
 FT /note= "Encoded by C76 in polymorphic variant"
 XX
 PN WO200035950-A2.
 XX
 PD 22-JUN-2000.
 XX
 PF 20-DEC-1999; 99WO-US30489.
 XX
 PR 18-DEC-1998; 98US-0215818.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Colpitts TL, Russell JE;
 XX
 DR WPI: 2000-442366/38.
 DR N-PSDB; AAA64846.
 XX
 PT Multimeric polypeptide antigen and antibody specific to the antigen are
 PT useful for diagnosing, detecting and treating breast cancer -
 PS Claim 1; Page 124; 124pp; English.
 XX

CC BU101 is a member of the uteroglobin protein family. The present
 CC sequence is the protein sequence for human BU101. The present
 CC invention relates to a multimeric polypeptide antigen, which comprises
 CC the present sequence and mammaglobin polypeptide (AAB13786).
 CC Mammaglobin is another uteroglobin protein. The presence of multimeric
 CC polypeptide antigen in a test sample can be used as the basis for a test
 CC to diagnose breast disease e.g. breast cancer, in a patient. The
 CC detection can be carried out using antibodies specific for the multimeric
 CC polypeptide antigen. The present sequence can either have a Pro or Leu
 CC residue at position 53, since the coding sequence has a single
 CC nucleotide T/C polymorphism at nucleotide position 254.

XX Sequence 90 AA;

Query Match 100.0%; Score 450; DB 21; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISSPLFKLSLAKEDAPPEAVAAKL 60

DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISSPLFKLSLAKEDAPPEAVAAKL 60

QY 61 GVKRCTDMSLQKRSLLAEVLVKILKCSY 90

DB 61 GVKRCTDMSLQKRSLLAEVLVKILKCSY 90

RESULT 6
 AAB07501
 ID AAB07501 standard; Protein; 90 AA.

AC AAB07501;

DT 20-OCT-2000 (first entry)

DE Amino acid sequence of a human BU101 polypeptide.

KW Human; BU101; breast disease.

OS Homo sapiens.

XX W0200041516-A2.

PD 20-JUL-2000.

PF 19-JAN-2000; 2000WO-US01309.

PR 19-JAN-1999; 99US-0233693.

PA (ABBO) ABBOTT LAB.

PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-rapp L;
 PI Russell JC, Scheffel CP, Stroupe SD;

DR WPI: 2000-475906/41.

DR N-PSDB; AAA58880.

PT Detecting presence of target BU101 polynucleotide in sample useful for
 PT detection of breast cancer, comprises contacting sample with
 PT BU101-specific polynucleotide and determining binding -

PS Claim 23; Page 125; 127pp; English.

CC The present sequence represents a BU101 polypeptide. The BU101 gene is
 CC transcribed from breast tissue. The specification describes a method for
 CC detecting the presence of a target BU101 polynucleotide in a test
 CC sample. The method comprises contacting the sample with at least one
 CC BU101-specific polynucleotide (AA58875-80), and detecting bound
 CC polynucleotides. The method and BU101 polynucleotides are useful for
 CC detecting the presence of BU101 polynucleotides. The methods may be
 CC used for the diagnosis of breast disease, indicated by the formation
 CC of complexes.

XX Sequence 90 AA;

Query Match 100.0%; Score 450; DB 21; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISSPLFKLSLAKEDAPPEAVAAKL 60

DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISSPLFKLSLAKEDAPPEAVAAKL 60

QY 61 GVKRCTDMSLQKRSLLAEVLVKILKCSY 90

DB 61 GVKRCTDMSLQKRSLLAEVLVKILKCSY 90

RESULT 7
 AAB03768
 ID AAB03768 standard; Protein; 90 AA.

AC AAB03768;

DT 06-OCT-2000 (first entry)

DE Human endometrial specific steroid-binding factor II protein sequence.

KW Endometrial specific steroid-binding factor; human; hESF; inflammation;
 KW asthma; rhinitis; cystic fibrosis; air way disease; neoplasia; atopy;
 KW eicosanoid level regulator; chemotaxis inhibitor; endometrial cancer; ss.

OS Homo sapiens.

XX US606724-A.

PD 23-MAY-2000.

PF 21-MAR-1997; 97US-0821451.

PR 21-MAR-1996; 96US-0014724.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Yu G, Gentz R, NI J;

DR WPI: 2000-375600/32.

DR N-PSDB; AAA59729.

PT Novel gene encoding human endometrial specific steroid-binding factor
 PT I, II and III which is useful for treating asthma, rhinitis, cystic
 PT fibrosis, airway disease and neoplasia -

PS Claim 1; Fig 2; 36pp; English.

CC This invention relates to nucleic acid molecules encoding portions of the
 CC human endometrial specific steroid-binding factors I, II, and III. Also
 CC included in the invention are hESF I, II, and III polypeptide sequences.
 CC The nucleotide sequence exhibit antiasthmatic, antiinflammatory,
 CC antiallergic, and cyostatic properties. The polynucleotides are used in
 CC gene therapy to express hESF I, II and III polypeptides in vivo to treat
 CC and/or prevent inflammation, asthma, rhinitis, cystic fibrosis, air way
 CC disease, neoplasia and atopy. The polynucleotides are also used to
 CC inhibit phospholipase A2 activity, bind polychlorinated biphenyls, reduce
 CC foreign protein antigenicity, inhibit monocyte and neutrophil chemotaxis
 CC and phagocytosis, inhibit platelet aggregation, regulate eicosanoid
 CC levels in the human uterus and control the growth of endometrial cells.
 CC The polynucleotides are also useful for detecting complementary
 CC polynucleotides as a diagnostic reagent. The hESF I, II and III
 CC polynucleotides are used to detect complementary polynucleotides such as
 CC a diagnostic reagent. Detection of a mutated form of hESF I, II and III
 CC associated with a dysfunction will provide a diagnostic tool that can
 CC define diagnosis of a disease or susceptibility to a disease which
 CC results from under-expression, over-expression or altered expression of
 CC hESF I, II and III e.g. a susceptibility to inherited asthma and

CC endometrial cancer. They are also useful for chromosome identification.
 CC The present sequence represents a hsf II protein sequence identified in
 CC the invention.

XX Sequence 90 AA;

Query Match 100.0%; Score 450; DB 21; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFPAPPAVAAKL 60
 DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFPAPPAVAAKL 60

OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKKCV 90
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKKCV 90

RESULT 8

AA84875
 ID AAY84875 standard; Protein; 90 AA.

XX AAY84875;

DT 08-AUG-2000 (first entry)

XX A human endometrial specific steroid-binding protein II.

XX Human; endometrial specific steroid-binding protein II; ESHPII;
 KM breast tumour; prostate cancer; gynaecological cancer; cancer;
 XX endometrial cancer; ovarian cancer; uterine cancer.

OS Homo sapiens.

XX WO200020043-A1.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US23252.

PR 05-OCT-1998; 98US-0103093.

PA (DIAD-) DIADEXUS LLC.

XX Macina RA;

DR WPI; 2000-303648/26.

DR N-PSDB; AAA14953.

XX Diagnosing, staging, monitoring, imaging and treating prostate and
 PT gynaecological cancers by measuring levels of endometrial specific
 XX steroid-binding protein (ESBP) II expression -
 PS Claim 6; Page 31-32; 35pp; English.

XX The present sequence represents a human endometrial specific steroid-
 CC binding protein (ESBP) II. The ESBPII protein is overexpressed in
 CC breast tumours. The specification describes a method for diagnosing
 CC prostate or a gynaecological cancer. The method comprises measuring
 CC levels of ESBPII in cells, tissues or body fluids of a patient, and
 CC comparing this to levels from a normal control, where a variance in
 CC levels indicates cancer. The method is used to diagnose, stage, monitor,
 CC image or treat prostate or gynaecological cancer. The gynaecological
 CC cancers include breast, endometrial, ovarian and uterine cancer.

XX Sequence 90 AA;

Query Match 100.0%; Score 450; DB 21; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFPAPPAVAAKL 60

DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFPAPPAVAAKL 60

OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKKCV 90
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKKCV 90

RESULT 9

AAG65989
 ID AAG65989 standard; Protein; 90 AA.

XX AAG65989;

DT 11-FEB-2002 (first entry)

XX Lipophilin B polypeptide.

XX Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
 KM cancer; B726P; Lipophilin B; mammaglobin.

XX Homo sapiens.

XX WO200175171-A2.

PD 11-OCT-2001.

PF 02-APR-2001; 2001WO-US10631.

PR 03-APR-2000; 2000US-194241P.

PR 20-JUL-2000; 2000US-219862P.

PR 27-JUL-2000; 2000US-221300P.

PR 18-DEC-2000; 2000US-256592P.

XX (CORI-) CORIXA CORP.

XX Houghton RL, Dillon DC, Molesh DA, Yu J, Zehentner B, Persing DH;

DR WPI; 2001-626449/72.

DR N-PSDB; AA167269.

XX Identifying tissue (tumour)-specific polynucleotides overexpressed in
 PT tissue of interest as compared to control tissue, for detecting cancer
 PT cells in patient, comprises DNA microarray analysis or quantitative
 PT polymerase chain reaction -
 XX Examples; Page 127; 127pp; English.

XX The invention relates to identifying tissue-specific polynucleotides (P)
 CC that involves performing a genetic subtraction to identify pool of (P)
 CC from tissue of interest (TI), performing DNA microarray analysis to
 CC identify first subset of polynucleotides (SP1) at least 2-fold over
 CC expressed in TI, and performing quantitative polymerase chain reaction
 CC (PCR) analysis on SP1 to identify second subset of (P). The method is
 CC useful for determining the presence or absence of a cancer cell in a
 CC patient, monitoring the progression of cancer in a patient using a
 CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
 CC urine or a tumour biopsy sample. The methods are useful for determining
 CC the presence or absence of or monitoring progression of prostate, breast,
 CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
 CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
 CC sequence represents the lipophilin B polypeptide.

XX Sequence 90 AA;

Query Match 100.0%; Score 450; DB 22; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFPAPPAVAAKL 60
 DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFPAPPAVAAKL 60

OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 10

ID AAE07518
 ID AAE07518 standard; Protein; 90 AA.

AC AAE07518;

DT 06-NOV-2001 (first entry)

DE Human lipophilin B protein.

KW Human; lipophilin B; cytosolic; vaccine; gene therapy; uteroglobin;
 KW cancer; breast; ovary; prostate.

OS Homo sapiens.

PN WO200158947-A1.

PD 16-AUG-2001.

PF 08-FEB-2001; 2001WO-US04439.

PR 11-FEB-2000; 2000US-0183495.

PR 28-JUN-2000; 2000US-0215735.

PA (CORI-) CORIXA CORP.

PI Carter D, Veddyck TS, Vallieve-Douglas J, Houghton RL, Dillon DC;

DR WPI; 2001-497069/54.

DR N-PSDB; AAD13756.

PT Novel isolated complex two lipophilin-like polypeptides linked by at
 PT least one disulfide bond, used to treat or prevent breast, ovarian or
 PT prostate cancer.

PS Example 5; Page 72; 91pp; English.

CC The invention relates to a complex comprising a lipophilin-like
 CC polypeptide linked by at least one disulfide bond to a second
 CC lipophilin-like polypeptide. Lipophilin-like protein are members of
 CC uteroglobin superfamily. Lipophilin-like proteins are useful in the
 CC preparation of vaccines. The complex containing lipophilin-like
 CC proteins are useful for treating or preventing breast, ovarian or
 CC prostate cancer. The complex is also used for determining the
 CC presence or absence of cancer in a patient, or monitor the progress
 CC of cancer in a patient. Lipophilin DNA is also useful in gene therapy.
 CC The present sequence is human lipophilin B protein.

SQ Sequence 90 AA;

Query Match 100.0%; Score 450; DB 22; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVTTALALCYQNAEFCPALVSELDFFISPLKSLAKDPAPVAARKL 60
 DB 1 MKLSVCLLVTTALALCYQNAEFCPALVSELDFFISPLKSLAKDPAPVAARKL 60

OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 11

ID AAB31681
 ID AAB31681 standard; Protein; 90 AA.

AC AAB31681;

XX 30-APR-2001 (first entry)
 DT An endometrial specific steroid binding factor II.

KW Human; endometrial specific steroid binding factor; hESF; hESFI; hESFII;
 KW hESFIII; inflammation; asthma; rhinitis; cystic fibrosis; airway disease;
 KW neoplasia; atopy; phospholipase A2; polychlorinated biphenyl; chemotaxis;
 KW phagocytosis; platelet aggregation; eicosanoid; endometrial cell.

OS Homo sapiens.

EH Key Location/Qualifiers
 FT Peptide 1..21
 FT /note= "signal peptide"

PN US6174992-B1.

PD 16-JAN-2001.

PF 08-MAR-1999; 99US-0263810.

PR 21-MAR-1996; 96US-0014724.

PR 21-MAR-1997; 97US-0821451.

PA (HUMA-) HUMAN GENOME SCI INC.

PI NI J, Yu G, Gentz R;

DR WPI; 2001-158477/16.

DR N-PSDB; AAF25213.

PT New human endometrial specific steroid binding factors, useful for
 PT treating and preventing inflammation, asthma, rhinitis, cystic
 PT fibrosis, airway disease, neoplasia and atopy

PS Claim 1; Fig 2; 36pp; English.

CC The present sequence represents a human endometrial specific steroid
 CC binding factor (hESF). The specification describes hESFI, hESFII, and
 CC hESFIII. hESFI, II and III polypeptides, and polynucleotides encoding
 CC them are useful for treating and preventing inflammation, asthma,
 CC rhinitis, cystic fibrosis, airway disease, neoplasia and atopy,
 CC inhibiting phospholipase A2 activity, binding polychlorinated
 CC biphenyls, reducing foreign protein antigenicity, inhibiting monocyte
 CC and neutrophil chemotaxis and phagocytosis, inhibiting platelet
 CC aggregation, regulating eicosanoid levels in the human uterus, and for
 CC controlling the growth of endometrial cells. hESF polypeptides and
 CC nucleotides are also useful for research, biological, clinical or
 CC therapeutic purposes.

SQ Sequence 90 AA;

Query Match 100.0%; Score 450; DB 22; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVTTALALCYQNAEFCPALVSELDFFISPLKSLAKDPAPVAARKL 60
 DB 1 MKLSVCLLVTTALALCYQNAEFCPALVSELDFFISPLKSLAKDPAPVAARKL 60

OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 12

ID ABB09634
 ID ABB09634 standard; Protein; 90 AA.

AC ABB09634;

DT 29-MAY-2002 (first entry)

XX Human endometrial specific steroid-binding factor (hESF) II.
 DE Human; endometrial specific steroid-binding factor; ESF.
 XX Prostatic steroid-binding protein; hESF I; hESF II; hESF III; asthma.
 KM Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT Protein /note= "signal peptide"
 FT Protein 22..90
 FT Protein /note= "mature protein"
 XX
 PN US6338948-B1.
 XX
 PD 15-JAN-2002.
 XX
 PF 30-MAY-2000; 2000US-0583169.
 XX
 PR 21-MAR-1996; 96US-014724P.
 PR 21-MAR-1997; 97US-082145I.
 PR 08-MAR-1999; 99US-0263810.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI NI J, Yu G, Gentz R;
 XX
 DR WPI; 2002-215019/27.
 DR N-PSDB; ABL41782.
 XX
 XX New antibody specific for human endometrial specific steroid-binding
 PT factor (hESF) III, useful for detecting hESF III protein in biological
 PT sample and to isolate or identify clones expressing the protein
 XX
 PS Disclosure; Fig 1; 36pp; English.
 XX
 XX The present sequence represents a endometrial specific steroid-binding
 CC factor (hESF) II. The full length protein has a molecular weight of
 CC 9.9 kDa. The protein has homology to rat prostatic steroid-binding
 CC protein C2. Antibodies which bind hESF proteins, such as hESF I, hESF II,
 CC and hESF III are useful for isolating or to identify clones expressing
 CC the polypeptides or to purify the polypeptides by affinity
 CC chromatography. Agonists and antagonists of hESF proteins are useful
 CC for treating and/or preventing susceptibility to asthma.
 CC
 XX
 SO Sequence 90 AA;
 Query Match 100.0%; Score 450; DB 23; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9, 2e-51;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKTSLVCLLYTALACCGAQAERCPALVSELDFFIFSEPLFKLSLAKFPAPPAVAAKL 60
 DB 1 MKTSLVCLLYTALACCGAQAERCPALVSELDFFIFSEPLFKLSLAKFPAPPAVAAKL 60
 QY 61 GVKRCFDMSLQKRSLLAEVLVILKKCSV 90
 DB 61 GVKRCFDMSLQKRSLLAEVLVILKKCSV 90
 RESULT 13
 ABB11907
 ID ABB11907 standard; peptide; 117 AA.
 AC ABB11907;
 XX
 DT 11-JAN-2002 (first entry)
 DE Human breast tumour-associated protein homologue, SPQ ID NO:2277.
 XX
 DE Human; cytokine; cell proliferation; cell differentiation; growth factor;
 XX haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KM

KM Inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 KM proliferation; metastasis; cancer; tumour haematopoietic disorder;
 KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KM chronic inflammatory condition; proliferative retinopathy;
 KM atherosclerosis; coronary heart disease; arterial ischaemia;
 KM bone disorder; osteoporosis; vascular growth disorder;
 KM tissue regeneration; wound healing; infection; immune disorder;
 KM cell culture; drug screening; gene therapy; antiinflammatory;
 KM antisthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KM cytosolic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
 KM antifungal; vulnery; antitumor.
 OS
 XX Homo sapiens.
 PN WO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US03800.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-457740/49.
 DR N-PSDB; ABA09151.
 XX
 XX Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer
 XX
 PS Claim 20; Page 275; 1963pp; English.
 XX
 XX Sequences ABB10981-ABB12330 represent 1150 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g. by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g. myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g. asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g. osteoporosis), and abnormal
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g. of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.

```

XX Sequence 117 AA:
SQ
Query Match 100.0%; Score 450; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 60
DB 28 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 87
OY 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 90
DB 88 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 117

RESULT 14
AAV48606
ID AAV48606 standard; Protein; 120 AA.
XX
AC AAV48606;
XX
DT 08-DEC-1999 (first entry)
XX
DE Human breast tumour-associated protein 67.
XX
KW Expressed sequence tag; EST; human; breast; cancer; gene therapy;
XX treatment; tumour; cytostatic; medicament.
XX
OS Homo sapiens.
XX
PN DE19813839-A1.
XX
PD 23-SEP-1999.
XX
PE 20-MAR-1998; 98DE-1013839.
XX
PR 20-MAR-1998; 98DE-1013839.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX WPI: 1999-528981/45.
XX DR N-PSDB; AA233666.
XX
PT Human nucleic acid sequences and protein products from tumor breast
XX tissue, useful for breast cancer therapy -
XX
PS Claim 22; 172; 188pp; German.
XX
CC This invention describes novel human nucleic acid sequences from tumor
XX breast tissue which have cytostatic activity. The nucleic acid sequences
XX can be used to produce and isolate full-length gene sequences. They can
XX be used to express proteins, which can be used as tools to find an
XX activity against breast cancer. The sequences can be used in sense or
XX antisense form. They are especially useful for medicaments for gene
XX therapy to treat breast cancer. AAV48540-Y48617 represent protein
XX fragments encoded by the expressed sequence tags described in the method
XX of the invention.
SQ Sequence 120 AA:
Query Match 100.0%; Score 450; DB 20; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 60
DB 31 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 90
OY 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 90

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DB 91 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 120

RESULT 15
AAE07521
ID AAE07521 standard; Protein; 90 AA.
XX
AC AAE07521;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human lipophilin B S11 3 3 protein.
XX
KW Human; lipophilin B S11 3 3; cytostatic; vaccine; gene therapy;
XX uteroglobin; cancer; breast; ovary; prostate.
XX
OS Homo sapiens.
XX
PN WO200158947-A1.
XX
PD 16-AUG-2001.
XX
PE 08-FEB-2001; 2001WO-US04439.
XX
PR 11-FEB-2000; 2000US-0183495.
XX
PR 28-JUN-2000; 2000US-0215735.
XX
PA (CORI-) CORIXA CORP.
XX
PI Carter D, Vedvick TS, Valilieve-Douglas J, Houghton RL, Dillon DC;
XX WPI: 2001-497069/54.
XX DR N-PSDB; AAD13761.
XX
PT Novel isolated complex two lipophilin-like polypeptides linked by at
XX least one disulfide bond, used to treat or prevent breast, ovarian or
XX prostate cancer -
XX
PS Example 5; Page 82; 91pp; English.
XX
CC The invention relates to a complex comprising a lipophilin-like
XX polypeptide linked by at least one disulfide bond to a second
XX lipophilin-like polypeptide. Lipophilin-like proteins are members of
XX uteroglobin superfamily. Lipophilin-like proteins are useful in the
XX preparation of vaccines. The complex containing lipophilin-like
XX proteins are useful for treating or preventing breast, ovarian or
XX prostate cancer. The complex is also used for determining the
XX presence or absence of cancer in a patient, or monitor the progress
XX of cancer in a patient. Lipophilin DNA is also useful in gene therapy.
XX The present sequence is human lipophilin B S11 3 3 protein.
SQ Sequence 90 AA:
Query Match 99.3%; Score 447; DB 22; Length 90;
Best Local Similarity 98.9%; Pred. No. 2.3e-50;
Matches 89; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 60
DB 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 60
OY 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 90
DB 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 90

```

Search completed: January 2, 2003, 14:54:21
Job time : 36 secs

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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:52:47 : Search time 12 Seconds

(without alignments)
311.072 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 450

Sequence: 1 MKLSVCLLVTLALCCYQAN.....LQKRSLIAEVLKILKCSV 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	450	100.0	90	1	LPBP_HUMAN
2	267	59.3	90	1	LPBP_HUMAN
3	206	45.8	111	1	PSC1_RAT
4	171	38.0	112	1	PSC2_RAT
5	110	24.4	91	1	UTER_HUMAN
6	102	22.7	91	1	UTER_RABIT
7	101	22.4	96	1	UTER_MOUSE
8	100	22.2	91	1	UTER_LEPCA
9	100	22.2	96	1	UTER_RAT
10	80.5	17.9	139	1	UGRI_MOUSE
11	75.5	16.8	93	1	UGRI_HUMAN
12	69	15.3	144	1	CYTE_MOUSE
13	66.5	14.8	3079	1	IRY2_YEAST
14	62.5	13.9	90	1	SY04_CHICK
15	62	13.8	105	1	FEL2_FELCA
16	62	13.8	149	1	CYTE_HUMAN
17	61.5	13.7	200	1	RISA_CHLPN
18	61	13.6	92	1	FELA_FELCA
19	60.5	13.4	1390	1	MET_HUMAN
20	60	13.3	123	1	CCRI_XENLA
21	59	13.1	261	1	YSC1_YERPE
22	59	13.1	270	1	ILIA_FELCA
23	58.5	13.0	646	1	GYRB_MYCA
24	58.5	13.0	1078	1	CYR7_BOVIN
25	58	12.9	140	1	FLAE_METJA
26	58	12.9	724	1	ME10_CAEBL
27	57.5	12.8	95	1	PSC3_RAT
28	57.5	12.8	591	1	VATA_CHLPN
29	57	12.7	282	1	D1L_DICDI
30	57	12.7	441	1	YDML_SCHPO
31	57	12.7	608	1	ALB1_SALSA
32	57	12.7	608	1	ALB2_SALSA
33	57	12.7	1107	1	YLK2_CAEBL

34	56.5	12.6	137	1	VGIL_EBV
35	56.5	12.6	262	1	X096_METJA
36	56.5	12.6	489	1	MONT_RAT
37	56.5	12.6	556	1	NU2M_PODAN
38	56.5	12.6	621	1	FX14_HUMAN
39	56.5	12.6	1080	1	CYAT_HUMAN
40	56	12.4	406	1	P152_HUMAN
41	56	12.4	446	1	AK_RICPR
42	56	12.4	1653	1	YFHM_ECOLI
43	55.5	12.3	76	1	RPOH_ARCFU
44	55.5	12.3	195	1	CNTE_CHICK
45	55.5	12.3	207	1	PLCR_PSEAE

ALIGNMENTS

RESULT 1	ID	LPBP_HUMAN	STANDARD:	PRT:	90 AA.
AC	095969				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Lipophilin B precursor (Secretoglobulin family 1D member 2).				
GN	SCGB1D2 OR LIPHB.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-99167354; PubMed-10066439;				
RA	Zhao C., Nguyen T., Yusifov T., Glasgow J.J., Lehrer R.I.;				
RT	"Lipophilins: human peptides homologous to rat prostalein.";				
RL	Biochem. Biophys. Res. Commun. 256:147-155(1999).				
CC	-1- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS. MAY ALSO BIND ESTRAMUSTINE, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.				
CC	MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.				
CC	-1- SUBCELLULAR LOCATION: Secreted (potential).				
CC	-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION WAS FOUND IN SKELETAL MUSCLE. EXPRESSED AS WELL IN THYMUS, TRACHEA, KIDNEY, STEROID RESPONSIVE TISSUES (PROSTATE, TESTIS, UTERUS, BREAST AND OVARY), AND SALIVARY GLAND.				
CC	-1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN SUBFAMILY.				
CC	-----				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL: AJ224172; CA11864.1; -				
DR	Genev; HGNC:18396; SCGB1D2.				
DR	InterPro: IPR000329; Uterogloblin.				
DR	Pfam: PF01099; Uterogloblin; 1.				
DR	PRINTS: PR00486; UTEROGLOBIN.				
DR	SMART: SM00096; UTG; 1.				
KW	Signal.				
FT	SIGNAL 1 21				POTENTIAL.
FT	CHAIN 22 90				LIPOPHILIN B.
FT	CHAIN 90 925				17BB555ED035D1AF CRC64;
SQ	SEQUENCE 90 AA; 9925 MW; 17BB555ED035D1AF CRC64;				
Query Match	100.0%;	Score 450;	DB 1;	Length 90;	
Best Local Similarity	100.0%;	Pred. No. 6,7e+45;			
Matches 90;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
OY	1 MKLSVCLLVTLALCCYQANAECPALVSELDFFFTSEBPLFKLSLAKFPDAPPAEVAVAL 60				
DB	1 MKLSVCLLVTLALCCYQANAECPALVSELDFFFTSEBPLFKLSLAKFPDAPPAEVAVAL 60				

OY 61 GVKRCTDQMSLOKRSILAELVLIKKCSV 90
 DB 61 GVKRCTDQMSLOKRSILAELVLIKKCSV 90

RESULT 2

LEPPA_HUMAN STANDARD; PRT; 90 AA.
 AC 095968;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lipophilin A precursor (Secretoglobin family 1D member 1).
 GN SCGB1D1 OR LIPHA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99167354; PubMed=10066439;
 RA Zhao C., Nguyen T., Yusuf T., Glasgow B.J., Lehrer R.I.;
 RT "Lipophilins: human peptides homologous to rat prostatein.";
 RL Biochem. Biophys. Res. Commun. 256:147-155(1999).
 RN [2]
 RP SEQUENCE OF 22-90, AND MASS SPECTROMETRY.
 RX MEDLINE=98385871; PubMed=9720917;
 RA Lehrer R.I., Xu G., Abduragimov A., Dinh N.N., Qu X.-D., Martin D.,
 Glasgow B.J.;
 RT "Lipophilin, a novel heterodimeric protein of human tears.";
 RL FEBS Lett. 432:163-167(1998).
 CC -1- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND
 ESTRADIOL. A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.
 CC MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.
 CC -1- SUBUNIT: HETERODIMER OF A LIPOPHILIN A AND A LIPOPHILIN C
 CC (MAMMAGLOBIN B) MONOMER ASSOCIATED HEAD TO HEAD.
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LACHRYMAL GLAND, THYMUS, KIDNEY,
 CC TESTIS, OVARY AND SALIVARY GLAND.
 CC -1- MASS SPECTROMETRY: MW=1574.69; METHOD=Electrospray; RANGE=22-90.
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN
 SUBFAMILY.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: AJ224171; CAA11863.1; -
 CC Genew: HGNC:18395; SCGB1D1.
 CC InterPro: IPR000329; Uteroglobln.
 CC Pfam: PF01099; Uteroglobln.1.
 CC PRINTS: PR00486; UTEROGLOBIN.
 CC SMART: SM00096; UTG; 1.
 CC Signal.
 CC KW SIGNAL.
 FT CHAIN 1 21 LIPOPHILIN A.
 FT SIGNAL 90
 SO SEQUENCE 90 AA; 9898 MW; DF2DF7565A87D34 CRC64;

Query Match 59.3%; Score 267; DB 1; Length 90;
 Best Local Similarity 60.2%; Pred. No. 6; Be-24;
 Matches 53; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQANAEFCPALVELDFEISPLFKLSIAKADPAEVAAYL 60
 DB 1 MKLSVCLLVLTALCCYQANAEFCPALVELDFEISPLFKLSIAKADPAEVAAYL 60
 OY 61 GVKRCTDQMSLOKRSILAELVLIKKCSV 88
 DB 61 GVKRCTDQMSLOKRSILAELVLIKKCSV 88

DB 61 EVKRCVDTMAYEKRVLIITKLGIAEK 88

RESULT 3

PSCI_RAT STANDARD; PRT; 111 AA.
 AC P02782; 063469;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Prostatic steroid-binding protein C1 chain precursor (Prostatein
 DE peptide C1).
 DE Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82220075; PubMed=6896362;
 RA Parker M.G., Needham M., White R.;
 RT "Prostatic steroid binding protein: gene duplication and steroid
 RT binding.";
 RL Nature 298:92-94(1982).
 RN [2]
 RP REVISIONS.
 RA Parker M.G.;
 RP Submitted (JUL-1983) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83234456; PubMed=6688048;
 RA Delaey B., Dirckx L., Peeters B., Voelckaert G., Mous J., Heyns W.,
 RA Rombaux W.;
 RT "The nucleotide sequence of cDNA complementary to the C1 component of
 RT rat prostatic binding protein.";
 RL Eur. J. Biochem. 133:645-649(1983).
 RN [4]
 RP SEQUENCE OF 24-111.
 RX MEDLINE=82164744; PubMed=7200013;
 RA Peeters B., Heyns W., Mous J., Rombaux W.;
 RT "Structural studies on rat prostatic binding protein. The primary
 RT structure of component C1 from subunit F.";
 RL Eur. J. Biochem. 123:55-62(1982).
 RN [5]
 RP SEQUENCE OF 24-111.
 RX MEDLINE=82075873; PubMed=7198120;
 RA Liao S., Chen C., Huang I.-Y.;
 RT "Prostate alpha-protein. Complete amino acid sequence of the
 RT component that inhibits nuclear retention of the androgen-receptor
 RT complex.";
 RL J. Biol. Chem. 257:122-125(1982).
 RN [6]
 RP SEQUENCE OF 13-65 FROM N.A.
 RA Delaey B., Rombaux W., Voelckaert G., Peeters B., Mous J., Heyns W.;
 RT "Identification of a complementary-DNA clone containing part of the
 RT sequence information for the C-1-polypeptide of rat prostatic binding
 RT protein.";
 RL Biochem. Soc. Trans. 10:51-51(1982).
 CC -1- FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY
 CC GLYCOPROTEIN OF VENTRAL PROSTATE GLAND.
 CC -1- SUBUNIT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED
 CC C1, C2 AND C3. THESE FORM COVALENT C1:C3 (F) AND C2:C3 (S)
 CC HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC
 CC (C1:C3/C3:C2) PROSTATEIN MOLECULES.
 CC -1- MISCELLANEOUS: THE HETERODIMER CAN BIND NON-POLAR STEROIDS,
 CC CHOLESTEROL AND A GROUP OF SMALL PROLINE-RICH PEPTIDES.
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN
 SUBFAMILY.
 CC -----
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DR EMBL: V01255; CAA24568.1; -
 DR EMBL: J00774; AAA41969.1; -
 DR EMBL: J00773; AAA41969.1; JOINED.
 DR EMBL: V01545; CAA24787.1; -
 DR PIR: A03252; BORT1.
 DR PIR: A42615; S42615.
 DR InterPro: IPR000329; Uteroglobln.
 DR Pfam: PF01099; Uteroglobln; 1.
 DR SMART: SM00096; UTRG; 1.
 DR PROSITE: PS00403; UTEROGLOBIN_1; FALSE_NEG.
 DR PROSITE: PS00404; UTEROGLOBIN_2; FALSE_NEG.
 KM Steroid-binding; signal.
 FT CHAIN 1 23
 FT SIGNAL 1 23
 FT PROSTATIC STEROID-BINDING PROTEIN C1
 FT CHAIN 1 23
 FT CONFLICT 5 5 K -> E (IN REF. 1; AAA41969).
 FT CONFLICT 15 15 A -> S (IN REF. 6).
 FT CONFLICT 17 18 CC -> GG (IN REF. 6).
 FT CONFLICT 74 74 N -> D (IN REF. 5).
 SQ SEQUENCE 111 AA; 12763 MW; 2CID11D003952945 CRC64;

Query Match 45.8%; Score 206; DB 1; Length 111.
 Best Local Similarity 49.5%; Pred. No. 8.4e-17; Matches 45; Conservative 14; Mismatches 30; Indels 2; Gaps 2;

QY 1 MKLSVLLVTLALCCYQANA-EFCPALVSELDFFFISEPLFKLSIAKFDAPPEAAK 59
 DB 4 IKSLICLLTI-LVCCCEANGQTLAGOVCOALDVTITFLNPBEELKRELEFDAPPEA 62

QY 60 LGVRCRDMSLDRSLIAEVLYKILKCSY 90
 DB 63 LEVRCVCDMSNGDRLVAAETLVYIFLECGV 93

RESULT 4
 PSC2_RAT
 ID PSC2_RAT STANDARD; PRT; 112 AA.
 AC P02781;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1988 (Rel. 06, last sequence update)
 DT 30-MAY-2000 (Rel. 39, last annotation update)
 DE Prostatic steroid-binding protein C2 chain precursor (Prostatein peptide C2).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBITaxID=10116;
 RX MEDLINE-87146484; PubMed-2881277;
 RA Delaey B., Dirckx L., Decourt J.-L., Claessens F., Peeters B., Rombauts W.;
 RT "Rat prostatic binding protein: the complete sequence of the C2 gene and its flanking regions";
 RL Nucleic Acids Res. 15:1627-1641(1987).
 RN 12
 RP SEQUENCE OF 21-112.
 RX MEDLINE-83209619; PubMed-6343081;
 RA Peeters B., Heyns W., Mous J., Rombauts W.;
 RT "Structural studies on rat prostatic binding protein. The primary structure of component C2 from subunit S.";
 RL Eur. J. Biochem. 132:669-679(1983).
 RL 13
 RP SEQUENCE OF 1-100 FROM N.A.
 RX MEDLINE-82220075; PubMed-6896362;
 RA Parker M., Needham M., White R.;
 RT "Prostatic steroid binding protein: gene duplication and steroid binding";
 RL Nature 298:92-94(1982).

CC -1- FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY GLYCOPROTEIN OF VENTRAL PROSTATE GLAND.
 CC -1- SUBUNIT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED C1, C2 AND C3. THESE FORM COVALENT C1-C3 (F) AND C2-C3 (S) HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC (C1-C3/C3-C2) PROSTATEIN MOLECULES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: LINKED BY THREE DISULFIDE BONDS TO C3.
 CC -1- MISCELLANEOUS: THE HETERODIMER CAN BIND NON-POLAR STEROIDS, CHOLESTEROL AND A GROUP OF SMALL PROLINE-RICH PEPTIDES.
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN SUBFAMILY.
 CC -----
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CC EMBL: X05034; CAA28708.1; -
 DR EMBL: V01256; CAA24569.1; -
 DR EMBL: J00776; AAA51641.1; -
 DR PIR: A03251; BORT2.
 DR PIR: A26671; A26671.
 DR InterPro: IPR000329; Uteroglobln.
 DR PROSITE: PS00403; UTEROGLOBIN_1; FALSE_NEG.
 DR PROSITE: PS00404; UTEROGLOBIN_2; FALSE_NEG.
 KM Steroid-binding; signal.
 FT CHAIN 1 20
 FT SIGNAL 1 20
 FT PROSTATIC STEROID-BINDING PROTEIN C2
 FT CHAIN 1 20
 FT MOD.RES 21 21 BLOCKED.
 FT DISULFID 28 28 INTERCHAIN (WITH C3) (PROBABLE).
 FT DISULFID 69 69 INTERCHAIN (WITH C3) (PROBABLE).
 FT DISULFID 92 92 INTERCHAIN (WITH C3) (PROBABLE).
 FT CONFLICT 26 26 MISSING (IN REF. 3).
 FT CONFLICT 88 88 I -> T (IN REF. 3).
 FT CONFLICT 96 112 VWLIQNPGRNFSSEIN -> YGK (IN REF. 3).
 SQ SEQUENCE 112 AA; 12828 MW; DA65A6A82677864 CRC64;

Query Match 38.0%; Score 171; DB 1; Length 112.
 Best Local Similarity 42.1%; Pred. No. 8.8e-13; Matches 40; Conservative 13; Mismatches 36; Indels 6; Gaps 2;

QY 1 MKLSVLLVTLALCCYQAN----AEFCPALVSELDFFFISEPLFKLSIAKFDAPPEA 55
 DB 1 MKLSICLLTI-LVCCCEANGQTLAGOVCOALDVTITFLNPBEELKRELEFDAPPEA 59

QY 56 VAAKLGVRCTDMSLDRSLIAEVLYKILKCSY 90
 DB 60 VEANLKYRCINKIMYGRSLMGSTLVFIMKCDV 94

RESULT 5
 UTER_HUMAN
 ID UTER_HUMAN STANDARD; PRT; 91 AA.
 AC P11684; Q9UCM4; Q9UCM2;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Clara cell phospholipid-binding protein precursor (CCPP) (Clara cells 10 kDa secretory protein) (CC10) (Uteroglobln) (Urine protein 1) (UP1).
 GN SCGB1A1 OR UGB OR CC10 OR CCSP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBITaxID=9606;
 RX MEDLINE-9606;
 RP SEQUENCE FROM N.A.
 RT TISSUE=Lung;

RX MEDLINE=89000784; PubMed=3167058;
 RA Singh G., Katyal S.L., Brown W.E., Phillips S., Kennedy A.L.,
 RA Anthony J., Squeglia N.;
 RT "Amino-acid and cDNA nucleotide sequences of human Clara cell 10 kDa
 RT protein."; Biochem. Biophys. Acta 950:329-337(1988).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=95250987; PubMed=7733299;
 RA Hay J.G., Danel C., Chu C., Crystal R.G.;
 RT "Human CC10 gene expression in airway epithelium and subchromosomal
 RT locus suggest linkage to airway disease."; Am. J. Physiol. 268:L565-L575(1995).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-18 FROM N.A.
 RX MEDLINE=93250776; PubMed=1284526;
 RA Wolf M., Klug J., Hackenberg R., Gessler M., Grzeschik K.-H.,
 RA Beato M., Suske G.;
 RT "Human CC10, the homologue of rabbit uteroglobin: genomic cloning,
 RT chromosomal localization and expression in endometrial cell lines."; Hum. Mol. Genet. 1:371-378(1992).
 RL [5]
 RP SEQUENCE OF 22-74.
 RC TISSUE=urine;
 RX MEDLINE=93016476; PubMed=1400743;
 RA Okutani R., Itoh Y., Hirata H., Kasahara T., Mukaida N., Kawai T.;
 RT "Simple and high-yield purification of urine protein 1 using
 RT immunofluorescence chromatography: evidence for the identity of urine
 RT protein 1 and human Clara cell 10-kilodalton protein."; J. Chromatogr. A 577:25-35(1992).
 RL [6]
 RP SEQUENCE OF 22-45.
 RC TISSUE=urine;
 RX MEDLINE=93009001; PubMed=1395029;
 RA Bernard A., Roels H., Lauwers R., Witters R., Gielens C.,
 RA Smaill A., Van Damme J., De Ley M.;
 RT "Human urinary protein 1: evidence for identity with the Clara cell
 RT protein and occurrence in respiratory tract and urogenital
 RT secretions."; Clin. Chim. Acta 207:239-249(1992).
 RL [7]
 RP SEQUENCE OF 22-33.
 RX MEDLINE=21648993; PubMed=11788998;
 RA Chafourti B., Stahlbom B., Tageson C., Lindahl M.;
 RT "Newly identified proteins in human nasal lavage fluid from
 RT non-smokers and smokers using two-dimensional gel electrophoresis and
 RT peptide mass fingerprinting."; Proteomics 2:112-120(2002).
 RL [8]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95393197; PubMed=7664082;
 RA Umland T.C., Swaminathan S., Singh G., Warty V., Furey W.,
 RA Pletcher J., Sax M.;
 RT "Structure of a human Clara cell phospholipid-binding protein-ligand
 RT complex at 1.9-A resolution."; Nat. Struct. Biol. 1:538-545(1994).
 RL [9]
 RP FUNCTION: BINDS PHOSPHATIDYLCHOLINE, PHOSPHATIDYLINOSITOL,
 CC POLYCHLORINATED BIPHENYLS (PCB) AND WEAKLY PROGESTERONE, POTENT
 CC INHIBITOR OF PHOSPHOLIPASE A2.
 CC [10]
 RP SUBUNIT: Homodimer: antiparallel disulfide-linked.
 CC [11]
 RP TISSUE SPECIFICITY: CLARA CELLS (NONCILIATED CELLS OF THE
 CC SURFACE EPITHELIUM OF THE PULMONARY AIRWAYS).
 CC [12]
 RP SIMILARITY: BELONGS TO THE UTEROGLIBIN FAMILY.
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 CC -----
 DR EMBL: X13197; CAA31584.1; -
 DR EMBL: U01101; AAA81885.1; -
 DR EMBL: U01102; AAA18297.1; -
 DR EMBL: BC004481; CAA04481.1; -
 DR EMBL: X59875; CAA42532.1; -
 DR PIR: J50036; J50036.
 DR PIR: S2651; S2651.
 DR HSSP: P02779; 10TG.
 DR GeneW: HGNC:12523; SCGB1A1.
 DR MIM: 192020; -
 DR InterPro: IPR003628; Uteroglbn_sub.
 DR InterPro: IPR000329; Uteroglbn.
 DR Pfam: PF01099; Uteroglbn_1.
 DR PRINTS: PR00486; UTEROGLBN.
 DR ProDom: PD012475; Uteroglbn_sub; 1.
 DR SMART: SM00096; UTG; 1.
 DR PROSITE: PS00403; UTEROGLBN_1; 1.
 DR PROSITE: PS00404; UTEROGLBN_2; 1.
 DR Phospholipase A2 inhibitor; Signal; Polymorphism.
 KW SIGNAL 1 21
 FT CHAIN 22 91 CLARA CELL PHOSPHOLIPID-BINDING PROTEIN.
 FT DISULFID 24 24 INTERCHAIN (WITH C-90').
 FT DISULFID 90 90 INTERCHAIN (WITH C-24').
 FT VARIANT 56 56 R->G (IN DBSNP:1802634).
 FT VARIANT 68 68 /FTID=VAR_012045.
 FT VARIANT 68 68 T->A (IN DBSNP:1802632).
 FT CONFLICT 24 24 /FTID=VAR_012046.
 FT CONFLICT 24 24 C->E (IN REF. 7).
 SQ SEQUENCE 91 AA; 9994 MW; FE65AC678F12ABD CRC64;
 Query Match 24.4%; Score 110; DB 1; Length 91;
 Best Local Similarity 31.0%; Pred. No. 7;le-06;
 Matches 26; Conservative 17; Mismatches 41; Indels 0; Gaps 0;
 QY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLKLSIAKDPAPPAVAKL 60
 DB 1 MKLAVTLTVTLALCCSSAALIC9SFQVITLMDPTSSYEAAMELSPDQDRNGA 60
 QY 61 GVKRCTDMSLQKRSLEIAEVYKI 84
 DB 61 QLKIVDTLPQKRPRESIIKIMEKI 84
 RESULT 6
 UTER_RABBIT
 ID UTER_RABBIT STANDARD: PRT; 91 AA.
 AC P02779;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Uteroglobin precursor (Blastokinin).
 GN SCGB1A1 OR UGB OR UGL.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_Taxid=9986;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83290960; PubMed=6309802;
 RA Bailey A., Atger M., Atger P., Cordon M.-A., Allison M., Vu Hai M.T.,
 RA Logeat F., Milgrom E.;
 RT "The rabbit uteroglobin gene. Structure and interaction with the
 RT progesterone receptor."; J. Biol. Chem. 258:10384-10389(1983).
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83220783; PubMed=6304644;
 RA Suske G., Wenz M., Cato A.C.B., Beato M.;

RT "The uteroglobin gene region: hormonal regulation, repetitive
 RT elements and complete nucleotide sequence of the gene.";
 RL Nucleic Acids Res. 11:2257-2271(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-83014990; PubMed-6956897;
 RA Menne C., Suske G., Arnenann J., Wenz M., Cato A.C.B., Beato M.;
 RT "Isolation and structure of the gene for the progesterone-inducible
 RT protein uteroglobin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:4853-4857(1982).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-83157105; PubMed-6299663;
 RA Chandra T., Bullock D.W., Moo S.L.C.;
 RT "Hormonally regulated mammalian gene expression: steady-state level
 RT and nucleotide sequence of rabbit uteroglobin mRNA.";
 RL DNA 1:19-26(1981).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-82275176; PubMed-6287481;
 RA Suske G., Menne C., Cato A., Wenz M., Beato M.;
 RT "Characterization and sequence analysis of interspersed repetitive
 RT DNA sequences transcribed in X. laevis embryos.";
 RL Prog. Clin. Biol. Res. 85:139-146(1982).
 RN [6]
 RP SEQUENCE OF 1-73.
 RX MEDLINE-79187160; PubMed-571719;
 RA Atger M., Mercier J.-C., Haze G., Fridlansky F., Milgrom E.;
 RT "N-terminal sequences of uteroglobin and its precursor.";
 RL Biochem. J. 177:985-988(1979).
 RN [7]
 RP SEQUENCE OF 22-91.
 RX MEDLINE-79042086; PubMed-568483;
 RA Ponstingl H., Nieto A., Beato M.;
 RT "Amino acid sequence of progesterone-induced rabbit uteroglobin.";
 RL Biochemistry 17:3908-3912(1978).
 RN [8]
 RP SEQUENCE OF 22-91.
 RX MEDLINE-79074850; PubMed-281700;
 RA Popp R.A., Foresman K.R., Wise L.D., Daniel J.C. Jr.;
 RT "Amino acid sequence of a progesterone-binding protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 75:5516-5519(1978).
 RN [9]
 RP REVISIONS TO 50-62 AND 67-71.
 RA Popp R.A., Foresman K.R., Wise L.D., Daniel J.C. Jr.;
 RT Submitted (OCT-1982) to the PIR data bank.
 RN [10]
 RP SEQUENCE OF 22-91 FROM N.A.
 RX MEDLINE-86056319; PubMed-2415398;
 RA de Haro M.S., Nieto A.;
 RT "Primary structure of rabbit lung uteroglobin as deduced from the
 RT nucleotide sequence of a cDNA.";
 RL FEBS Lett. 193:247-249(1985).
 RN [11]
 RP SEQUENCE OF 39-77 FROM N.A.
 RX MEDLINE-81021016; PubMed-7417250;
 RA Chandra T., Moo S.L.C., Bullock D.W.;
 RT "Cloning of the rabbit uteroglobin structural gene.";
 RL Biochem. Biophys. Res. Commun. 95:197-204(1980).
 RN [12]
 RP SEQUENCE OF 53-72 FROM N.A.
 RX MEDLINE-80241888; PubMed-6156676;
 RA Atger M., Perricaudet M., Tjolliaas P., Milgrom E.;
 RT "Bacterial cloning of the rabbit uteroglobin structural gene.";
 RL Biochem. Biophys. Res. Commun. 93:1082-1088(1980).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (1.64 ANGSTROMS).
 RX MEDLINE-89199637; PubMed-2704039;
 RA Bally R., Delettre J.;
 RT "Structure and refinement of the oxidized P21 form of uteroglobin at
 RT 1.64-A resolution.";
 RL J. Mol. Biol. 206:153-170(1989).
 RN [14]

RP X-RAY CRYSTALLOGRAPHY (1.34 ANGSTROMS).
 RX MEDLINE-88011213; PubMed-3656405;
 RA Morize I., Surcouf E., Vaney M.C., Epelboin Y., Buehner M.,
 RA Fridlansky F., Milgrom E., Moron J.-P.;
 RT "Refinement of the C222(1) crystal form of oxidized uteroglobin at
 RT 1.34-A resolution.";
 RL J. Mol. Biol. 194:725-739(1987).
 RN [15]
 RP STRUCTURE BY NMR OF 39-68.
 RX MEDLINE-94297152; PubMed-8025221;
 RA Imptola S., Pastore A., Mammì S., Peglion E.;
 RT "Conformation and molecular dynamics calculations on uteroglobin
 RT fragment 18-47.";
 RL Biopolymers 34:773-782(1994).
 CC -1- FUNCTION: UTEROGLIBIN BINDS PROGESTERONE SPECIFICALLY AND WITH
 CC HIGH AFFINITY. IT MAY REGULATE PROGESTERONE CONCENTRATIONS
 CC REACHING THE BLATOCYST. IT IS ALSO A POTENT INHIBITOR OF
 CC PHOSPHOLIPASE A2.
 CC -1- SUBUNIT: Homodimer; antiparallel disulfide-linked.
 CC -1- INDUCTION: UTEROGLIBIN, SYNTHESIZED IN THE UTERUS AND LUNG, IS
 CC SECRETED BY THE UTERUS UPON INDUCTION BY PROGESTERONE.
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLIBIN FAMILY.
 CC -----
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 CC -----
 DR EMBL: K01657; AAA31497.1; -;
 DR EMBL: J00689; AAA31495.1; -;
 DR EMBL: J00688; AAA31495.1; JOINED.
 DR EMBL: X01423; CAA25669.1; -;
 DR EMBL: M32012; AAA31500.1; -;
 DR EMBL: M25090; AAA31500.1; JOINED.
 DR EMBL: M27564; AAA31496.1; -;
 DR EMBL: M25057; AAA31498.1; -;
 DR EMBL: M25038; AAA31499.1; -;
 DR PIR: A03249; UGRB.
 DR PDB: 1UTG; 15-OCT-92.
 DR PDB: 2UTG; 15-OCT-89.
 DR InterPro: IPR003628; Uteroglbn sub.
 DR InterPro: IPR000329; Uteroglobin.
 DR Pfam: PF01099; Uteroglobin_1.
 DR PRINTS: PR00486; UTEROGLIBIN.
 DR PRODOM: PD012475; Uteroglbn_sub; 1.
 DR SMART: SM00096; UTG; 1.
 DR PROSITE: PS00403; UTEROGLIBIN_1; 1.
 DR PROSITE: PS00404; UTEROGLIBIN_2; 1.
 KW Phospholipase A2 inhibitor; Steroid-binding; Signal; 3D-structure.
 FT STGNAL 1 21
 FT CHAIN 22 91
 FT DISULFID 24 24 INTERCHAIN (WITH C-90').
 FT DISULFID 90 90 INTERCHAIN (WITH C-24').
 FT CONFLICT 6 6 T -> F (IN REF. 6).
 FT CONFLICT 16 16 C -> G (IN REF. 6).
 FT CONFLICT 46 46 L -> V (IN REF. 5).
 FT CONFLICT 67 68 DS -> NT (IN REF. 12).
 FT CONFLICT 82 82 E -> Q (IN REF. 7).
 FT HELIX 39 47
 FT HELIX 48 49
 FT TURN 53 66
 FT HELIX 67 68
 FT TURN 71 85
 FT HELIX 86 86
 FT TURN 88 90
 FT HELIX 91 91
 SO SEQUENCE 91 AA; 9983 MW; 0C1978AN15D550CA CRC64;
 Query Match 22.7%; Score 101; DB 1; Length 91;
 Best Local Similarity 30.2%; Pred. No. 5,9e-05;

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CC -----
DR EMBL; M25609; AAA30960.1; -
DR PIR; A23825; UGRBL.
DR HSSP; P02779; UTRG.
DR InterPro; IPR003628; Uteroglobin-sub.
DR InterPro; IPR000329; Uteroglobin.
DR Pfam; PF01099; Uteroglobin.1.
DR PRINTS; PR00486; UTEROGLOBIN.
DR ProDom; PD012475; Uteroglobin-sub; 1.
DR SMART; SM00096; UTRG; 1.
DR PROSITE; PS00403; UTEROGLOBIN.1; 1.
DR PROSITE; PS00404; UTEROGLOBIN.2; 1.
KW Phospholipase A2 inhibitor; Steroid-binding; Signal.
FT SIGNAL 1 21
FT CHAIN 22 91 UTEROGLOBIN.
FT DISULFID 24 24 INTERCHAIN (WITH C-90').
FT DISULFID 90 90 INTERCHAIN (WITH C-24').
SQ SEQUENCE 91 AA; 9879 MW; 587614DAE9E4820F CRC64;

Query Match 22.2%; Score 100; DB 1; Length 91;
Best Local Similarity 30.2%; Pred. No. 0.0001;
Matches 26; Conservative 16; Mismatches 44; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALACQYANAEFCPALVSELDFFISPEFLSLAKDAPAEVAARL 60
DB 1 MKLTITLVLTALACSPASAGICPGFAHVIEMLLGTSSVTSLSKEFGPDAMDAGM 60
QY 61 GYKRCIDMSLQKRSLLAEVLYKILK 86
DB 61 OMKRVLDPLPQTRRNIIRLTERIKV 86

RESULT 9
UTER_RAT STANDARD; PRT; 96 AA.
AC P17559;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Clara cell phospholipid-binding protein precursor (CCBP) (Clara cells
DE 10 kDa secretory protein) (CC10) (Uteroglobin) (PCB-binding protein).
GN SCGB1A1 OR UGB OR CC10 OR UTRG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN NCBI_TaxId=10116;
RN SEQUENCE FROM N.A.
RA Katyal S.L., Singh G., Brown W.E., Kennedy A.L., Squeglia N.,
RA Wong-Chong M.-L.;
RT "Clara cell secretory (10 kDa) protein: amino acid and cDNA
RT nucleotide sequences and developmental expression";
RL Prog. Respir. Res. 25:29-35(1990).
RN [2]
RX MEDLINE=90324266; PubMed=2115524;
RA Nordlund-Moeller L., Andersson O., Ahlgren R., Schilling J.,
RA Gillner M., Gustafsson J.-A., Lund J.;
RT "Cloning, structure, and expression of a rat binding protein for
RT polychlorinated biphenyls. Homology to the hormonally regulated
RL J. Biol. Chem. 265:12690-12693(1990).
RN [3]
RX SEQUENCE OF 1-18 FROM N.A.
RX MEDLINE=90727298; PubMed=2349092;
RA Hagen G., Wolf M., Katyal S.L., Singh G., Beato M., Suske G.;

RT "Tissue-specific expression, hormonal regulation and 5'-flanking gene
RT region of the rat Clara cell 10 kDa protein: comparison to rabbit
RT uteroglobin".
RL Nucleic Acids Res. 18:2939-2946(1990).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=92219263; PubMed=1560460;
RA Umland T.C., Swaminathan S., Purey W., Singh G., Fletcher J., Sax M.;
RT "Refined structure of rat Clara cell 17 kDa protein at 3.0-A
RT resolution".
RL J. Mol. Biol. 224:441-448(1992).
RN [5]
RX STRUCTURE BY NMR.
RX MEDLINE=96069785; PubMed=7583672;
RA Haerd T., Barnes H.J., Larsson C., Gustafsson J.-A., Lund J.;
RT "Solution structure of a mammalian PCB-binding protein in complex
RT with a PCB".
RL Nat. Struct. Biol. 2:983-989(1995).
CC -1- FUNCTION: BINDS PHOSPHATIDYLCHOLINE, PHOSPHATIDYLINOSITOL,
CC POLYCHLORINATED BIPHENYLS (PCB) AND WEAKLY PROGESTERONE, POTENT
CC INHIBITOR OF PHOSPHOLIPASE A2.
CC -1- SUBUNIT: Homodimer; antiparallel disulfide-linked.
CC -1- TISSUE SPECIFICITY: CLARA CELLS (NON-ILATED CELLS OF THE
CC SURFACE EPITHELIUM OF THE PULMONARY AIRWAYS).
CC -1- INDUCTION: BY GLUCOCORTICOIDS.
CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY.
CC -----
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CC -----
DR EMBL; J05536; AAA41817.1; -
DR EMBL; X51318; CAA35701.1; -
DR PIR; A36581; A36581.
DR PIR; S10185; A36581.
DR PIR; S21676; S21676.
DR PDB; 1CCD; 31-JAN-94.
DR PDB; 1UTR; 07-DEC-95.
DR InterPro; IPR003628; Uteroglobin-sub.
DR InterPro; IPR000329; Uteroglobin.
DR Pfam; PR00486; UTEROGLOBIN.1.
DR PRINTS; PR00486; UTEROGLOBIN.
DR ProDom; PD012475; Uteroglobin-sub; 1.
DR SMART; SM00096; UTRG; 1.
DR PROSITE; PS00403; UTEROGLOBIN.1; 1.
DR PROSITE; PS00404; UTEROGLOBIN.2; 1.
KW Phospholipase A2 inhibitor; Signal; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 96 CLARA CELL PHOSPHOLIPID-BINDING PROTEIN.
FT DISULFID 24 24 INTERCHAIN (WITH C-90').
FT DISULFID 90 90 INTERCHAIN (WITH C-24').
FT TURN 21 22
FT HELIX 25 34
FT TURN 35 36
FT HELIX 39 46
FT TURN 47 49
FT HELIX 53 68
FT HELIX 71 84
FT TURN 85 86
FT TURN 88 90
SQ SEQUENCE 96 AA; 10449 MW; 1A12988677B9EBEF CRC64;

Query Match 22.2%; Score 100; DB 1; Length 96;
Best Local Similarity 25.9%; Pred. No. 0.00011;
Matches 22; Conservative 22; Mismatches 41; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALACQYANAEFCPALVSELDFFISPEFLSLAKDAPAEVAARL 60
DB 1 MKLTITLVLTALACSPASAGICPGFAHVIEMLLGTSSVTSLSKEFGPDAMDAGM 60

OY 61 GVKRCTDMSLOKRSIAEVLVKIL 85
 Db 61 QLRRLVDTLPQETRINIVKLEKIL 85

RESULT 10

UGR1_MOUSE STANDARD: PRT; 139 AA.
 ID UGR1_MOUSE
 AC Q920H1; Q920H2; Q920H3;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A member 2).
 GN SCGB3A2 OR UGRP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539178; PubMed=11682631;
 RA Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.;
 RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor.";
 RL Mol. Endocrinol. 15:2021-2036(2001).
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; A, B and C (shown here); are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung.
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. UGRP SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF274959; AAL25708.1; -
 CC EMBL; AF274960; AAL25709.1; -
 CC EMBL; AF274961; AAL25710.1; -
 CC InterPro: IPR000329; Uteroglobin.
 CC Pfam; PF01099; Uteroglobin; 1.
 CC Signal; Alternative splicing.
 CC SIGNAL 1 21 POTENTIAL.
 CC CHAIN 22 139 UTEROGLOBIN-RELATED PROTEIN 1.
 CC VARSPLIC 107 139 VSVLFPMICAYPRDSKQTFATFERVEQSKL -> EALS
 CC VARSPLIC 85 91 VITICSY -> EALSHLY (IN ISOFORM A).
 CC VARSPLIC 92 139 MISSING (IN ISOFORM A).
 CC SEQUENCE 139 AA; 15431 MW; 8A2FB080B416554 CRC64;

Query Match 17.9%; Score 80.5; DB 1; Length 139;
 Best Local Similarity 27.6%; Pred. No. 0.027;
 Matches 27; Conservative 19; Mismatches 35; Indels 17; Gaps 5;

OY 1 MKLSVCLLVTLALCCYQANA-----EFCPALVSELDFFFISEPLFKLSLAKFDA 51
 Db 1 MKLVSIFLVTIGICGYATALLINRLPVDKLPVPLDILPSF---DPL-KMLKLTGI 56
 OY 52 PPEAVAAKLGVRCTDMSLOKRSIAEVLVKILKKS 89
 Db 57 SVEHLVLT--GLKRCVDELGPASEAVKRLVLI--CS 90

RESULT 11

UGR1_HUMAN STANDARD: PRT; 93 AA.
 ID UGR1_HUMAN
 AC Q96P1;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A member 2).
 GN SCGB3A2 OR UGRP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539178; PubMed=11682631;
 RA Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.;
 RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor.";
 RL Mol. Endocrinol. 15:2021-2036(2001).
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung.
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. UGRP SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; AF313455; AAL26215.1; -
 CC Genew; HGNC:18391; SCGB3A2.
 CC MIM; 606531; -
 CC Signal.
 CC SIGNAL 1 21 POTENTIAL.
 CC CHAIN 22 93 UTEROGLOBIN-RELATED PROTEIN 1.
 CC SEQUENCE 93 AA; 10161 MW; FB4BFRAC2BF3718 CRC64;

Query Match 16.8%; Score 75.5; DB 1; Length 93;
 Best Local Similarity 27.0%; Pred. No. 0.067;
 Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;

OY 1 MKLSVCLLVTLALCCYQANA-----EFCPALVSELDFFFISEPLFKLSLAKF 49
 Db 1 MKLVITFLVTISLSYATFLINKVPLPVDKLAPLDNITLPPM---DPL-KLLKTL 56
 OY 50 DAPPEAVAAKLGVRCTDMSLOKRSIAEVLVKILKKS 89
 Db 57 GISVEHLVE--GLKRCVDELGP-----ASEAVKLLLEALS 90

RESULT 12
 CYTE_MOUSE STANDARD: PRT; 144 AA.
 ID CYTE_MOUSE
 AC O89098;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cystatin F precursor (leukocystatin) (cystatin 7) (cystatin-like metastasis-associated protein) (CMAP).
 GN CMT7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98298157; PubMed=9632704;

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RA Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,
RA Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque S.,
RA Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.,
RT "Leucocystatin, a new class II cystatin expressed selectively by
RT hematopoietic cells.",
RL J. Biol. Chem. 273:16400-16408(1998).
CC -1- FUNCTION: INHIBITS PAPAIN AND CATHEPSIN L BUT WITH AFFINITIES
CC LOWER THAN OTHER CYSTATINS. MAY PLAY A ROLE IN IMMUNE REGULATION
CC THROUGH INHIBITION OF A UNIQUE TARGET IN THE HEMATOPOIETIC SYSTEM.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: BELONGS TO THE CYSTATIN FAMILY.
-----
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-----
DR EMBL: AF031826; AAC40140.1; -
DR EMBL: AF031825; AAC40139.1; -
DR HSSP: P01034; I696.
DR MGD: MGI:1298217; Cst7.
DR InterPro: IPR000010; Cystatin.
DR Pfam: PF00031; cystatin; 1.
DR SMART: SM00043; cy: 1.
DR PROSITE: PS00287; CYSTATIN; FALSE_NEG.
KW Thiol protease inhibitor; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 144 CYSTATIN F.
FT ACT_SITE 36 36 REACTIVE SITE.
FT SITE 80 84 SECONDARY AREA OF CONTACT.
FT DISULFID 98 109 BY SIMILARITY.
FT DISULFID 123 143 BY SIMILARITY.
SQ SEQUENCE 144 AA; 16380 MW; B5837334C1B4A89C CRC64;

Query Match 15.3%; Score 69; DB 1; Length 144;
Best Local Similarity 27.0%; Pred. No. 0.57;
Matches 24; Conservative 22; Mismatches 25; Indels 18; Gaps 5;

QY 8 LVLTLALCCYQANA-----EFCPA-LVSELDFFISEPLFKLSLAKFPDPAVNAKL 60
DB 3 LAILLALCCLTSDHGARPDPFCSDLISSV-----KPGFPRTI-ETNNPGVLKAAKH 54
QY 61 GYAR---CTDOMSLQKRSILAENVLYKLK 86
DB 55 SVEKFNCTNDIFLEKSHVSKALVQYVK 83

RESULT 13
ID IRA2_YEAST STANDARD; PRT; 3079 AA.
AC P19158; Q08239;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Inhibitory regulator protein IRA2.
GN IRA2 OR GLC4 OR CCS1 OR YOL081W OR O0985.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID:4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90318397; PubMed-2164637;
RA Tanaka K., Nakafuku M., Tamanoi F., Kaziro Y., Matsumoto K., Toh-E A.;
RT "IRA2, a second gene of Saccharomyces cerevisiae that encodes a
RT protein with a domain homologous to mammalian ras GTPase-activating
RT protein.",
RL Mol. Cell. Biol. 10:4303-4313(1990).
RN [2]
RP SEQUENCE OF 1-2423 FROM N.A.

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RC STRAIN-S288C / FY1679;
RX MEDLINE-95208358; PubMed-7900427;
RA Zumstein E., Griffin H., Schweizer M.;
RT "Sequence of a 10.27 kb segment on the left arm of chromosome XV from
RT Saccharomyces cerevisiae includes part of the IRA2 gene and a
RT putative new gene.",
RL Yeast 10:1383-1387(1994).
RN [3]
RP SEQUENCE OF 1982-3079 FROM N.A.
RX MEDLINE-97321807; PubMed-9178509;
RA Tzermia M., Katsoulou C., Alexandraki D.;
RT "Sequence analysis of a 33.2 kb segment from the left arm of yeast
RT chromosome XV reveals eight known genes and ten new open reading
RT frames including homologues of ABC transporters, inositol
RT phosphatases and human expressed sequence tags.",
RL Yeast 13:583-589(1997).
RN [4]
RP IDENTIFICATION OF CCS1 AS IRA2.
RX Bussereau F., Dupont C.H., Boy-Marcotte E., Mallet L., Jacquet M.;
RT "The CCS1 gene from Saccharomyces cerevisiae which is involved in
RT mitochondrial functions is identified as IRA2 an attenuator of RAS1
RT and RAS2 gene products.",
RL Curr. Genet. 21:325-329(1992).
CC -1- FUNCTION: INHIBITORY REGULATOR OF THE RAS-CYCCLIC AMP PATHWAY.
CC STIMULATES THE GTPASE ACTIVITY OF RAS PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 RAS-GAP DOMAIN.
-----
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-----
DR EMBL: M33779; AAA34710.1; -
DR EMBL: X83121; CAA58201.1; -
DR EMBL: X75449; CAA53202.1; -
DR EMBL: Z74823; CAA99093.1; -
DR PIR: S11190; R8BY12.
DR SGD: S0005441; IRA2.
DR InterPro: IPR001936; RASGAP.
DR Pfam: PF00616; RASGAP; 1.
DR SMART: SM00323; RASGAP; 1.
DR PROSITE: PS00509; RAS_GTPASE_ACTIV_1; 1.
DR PROSITE: PS50018; RAS_GTPASE_ACTIV_2; 1.
KW GTPase activation.
FT DOMAIN 1701 1890 RAS-GAP.
FT DOMAIN 399 409 POLY-SER.
FT DOMAIN 412 416 POLY-SER.
FT DOMAIN 520 528 POLY-ALA.
FT DOMAIN 2469 2472 POLY-LEU.
FT CONFLICT 2317 2317 I -> K (III REF. 3).
SQ SEQUENCE 3079 AA; 351631 MW; 651EB.A2EEBA479C0 CRC64;

Query Match 14.8%; Score 66.5; DB 1; Length 3079;
Best Local Similarity 32.3%; Pred. No. 24;
Matches 20; Conservative 9; Mismatches 18; Indels 15; Gaps 2;

QY 23 FCPALVS---ELDFFISEPLFKLSLAK-----FDAPPEAVNAKLGVKRCRD 67
DB 1654 FCPALVSPDSNITIDISHSEKRFIFSLAKYIQNANGSEWFRMPALCSQDKFLKCSQD 1913
QY 68 QM 69
DB 1914 RI 1915

RESULT 14
ID SY04_CHICK STANDARD; PRT; 90 AA.
AC Q90826; Q910C9;

```

DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Small inducible cytokine A4 homolog precursor (Macrophage inflammatory
 DE protein 1-beta homolog).
 GN SCYA4.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=bone marrow;
 RX MEDLINE=95369710; PubMed=7642115;
 RA Petrenko O., Enrietto P.J.;
 RT "Isolation of a cDNA encoding a novel chicken chemokine homologous to
 RT mammalian macrophage inflammatory protein-1 beta.";
 RL Gene 160:305-306(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hughes S.M., Bumstead N.;
 RT "Mapping of the gene encoding the chicken homologue of the mammalian
 RT chemokine SCYA4.";
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 14-90 FROM N.A.
 RA Petrenko O., Enrietto P.J.;
 RT Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES
 CC (BY SIMILARITY)
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
 CC C-C) (CHEMOKINE CC).
 CC -----
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 CC -----
 CC EMBL: L34553; AAA48747.1; -;
 CC EMBL: AJ243034; CAB45103.1; -;
 CC DR HSP: P13236; IHOM.
 CC DR InterPro: IPR000827; CC=chemkine_sml.
 CC DR InterPro: IPR001811; Chemokine_IL8.
 CC DR Pfam: PF00048; IL8; 1.
 CC DR SMART: SM00199; SCY; 1.
 CC DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
 CC KW Cytokine; Chemotaxis; Signal.
 CC FT SIGNAL 1 21 BY SIMILARITY.
 CC FT CHAIN 22 90 SMALL INDUCIBLE CYTOKINE A4 HOMOLOG.
 CC FT DISULFID 32 56 BY SIMILARITY.
 CC FT DISULFID 33 72 BY SIMILARITY.
 CC FT CONFLICT 87 87 M -> L (IN REF. 1).
 CC FT CONFLICT 87 87
 CC SQ SEQUENCE 90 AA; 9987 MW; 50AF9679A267408F CRC64;
 Query Match 13.9%; Score 62.5; DB 1; Length 90;
 Best Local Similarity 33.3%; Pred. No. 2;
 Matches 16; Conservative 6; Mismatches 17; Indels 9; Gaps 1;
 QY 1 MKLSVCLLVLTALCCYQANA-----EPCPALVSELDFFFISE 39
 DB 1 MKVSAALAVLLALTCYQTSAPVGSDDPTSCCTTISQLPFSVAD 48
 RESULT 15
 FE12_FE1CA STANDARD; PRT; 109 AA.
 AC P30440;

DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Major allergen I polypeptide chain 2 precursor (Allergen Fel d 1-B)
 DE (Fel d I-B) (Allergen Cat-1) (Ag4) (f01).
 GN CH2.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-100.
 RX MEDLINE=92052157; PubMed=1946388;
 RA Morgenstern J.P., Griffith I.J., Brauer A.W., Rogers B.L.,
 RA Bond J.F., Chapman M.D., Kuo M.-C.;
 RT "Amino acid sequence of fel d1, the major allergen of the domestic
 RT cat: protein sequence analysis and cDNA cloning";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9690-9694(1991).
 RN [2]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS.
 RC TISSUE=Liver;
 RX MEDLINE=92241678; PubMed=1572548;
 RA Griffith I.J., Craig S., Pollock J., Yu X.-B., Morgenstern J.P.,
 RA Rogers B.L.;
 RT "Expression and genomic structure of the genes encoding f01, the
 RT major allergen from the domestic cat.";
 RL Gene 113:263-268(1992).
 RN [3]
 RP SEQUENCE OF 18-37, AND CHARACTERIZATION.
 RX MEDLINE=91287714; PubMed=1712068;
 RA Duffort O.A., Carreira J., Nitti G., Polo F., Lombardero M.;
 RT "Studies on the biochemical structure of the major cat allergen Felis
 RT domesticus I.";
 RL Mol. Immunol. 28:301-309(1991).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=84265679; PubMed=6747135;
 RA Lelerman K., Oman J.L. Jr.;
 RT "Cat allergen 1: Blochemical, antigenic, and allergenic properties.";
 RL J. Allergy Clin. Immunol. 74:147-153(1984).
 CC -1- SUBUNIT: HETEROTETRAMER COMPOSED OF TWO NON-COVALENTLY LINKED
 CC DISULFIDE-LINKED HETERODIMER OF CHAINS 1 AND 2.
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; a long form/CH2 (shown here), a
 CC short form/CH2S and a truncated form/CH2ST; may be produced by
 CC alternative splicing.
 CC -1- TISSUE SPECIFICITY: THE LONG FORM IS PREFERENTIALLY EXPRESSED IN
 CC THE SALIVARY GLAND, WHILE THE SHORT FORM IS PREFERENTIALLY
 CC EXPRESSED IN THE SKIN.
 CC -1- DISEASE: MAJOR ALLERGEN PRODUCED BY THE DOMESTIC CAT.
 CC -----
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 CC or send an email to license@sib-sib.ch)
 CC -----
 CC EMBL: M77341; AAC41616.1; -;
 CC DR EMBL: X62478; CAA44345.1; -;
 CC DR PIR: JC1127; JC1127.
 CC DR PIR: JC1145; JC1145.
 CC KW Allergen; Glycoprotein; Signal; Polymorphism; Alternative splicing.
 CC FT SIGNAL 1 17
 CC FT CHAIN 18 109 MAJOR ALLERGEN I POLYPEPTIDE CHAIN 2.
 CC FT CARBOHYD 50 50 N-LINKED (GLCNAc...)
 CC FT VARSPLIC 82 109 TTSSSKCKMGKAVONTVEDLKLNTLGR -> PSTNIMAVK
 CC FT VARSPLIC 82 89 QFRP (IN ISOFORM CH2ST).
 CC FT VARSPLIC 72 72 TTSSSKND -> IAINRY (IN ISOFORM CH2S).
 CC FT VARSPLIC 72 72 I -> L (IN CH2LV).
 CC FT VARSPLIC 74 75 I -> V (IN CH2SV).
 CC FT VARSPLIC 74 75 RV -> KF (IN CH2SV).
 CC FT VARSPLIC 91 91 M -> T (IN CH2LV).
 FT VARIANT

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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:53:42 ; Search time 17 Seconds

(without alignments)
508.947 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 450
Sequence: 1 MKLSVCLLVTLALCCYQAN.....LQKRSLIAEVLVKKCSV 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	45.8	111	1 BOR1	prostatic steroid-
2	177	39.3	95	2 S68231	FHG22 protein prec
3	166.5	37.0	98	1 BOR2	prostatic steroid-
4	110	24.4	91	2 JS0036	Clara cell 10K pro
5	102	22.7	91	1 UGRB	uteroglobin precu
6	101	22.4	96	1 UGMS	uteroglobin precu
7	100	22.2	96	2 A36581	polychlorinated bi
8	97	21.6	91	1 UGRB	uteroglobin precu
9	83.5	18.6	113	2 JC2026	cell specific 10K
10	77.5	17.2	94	2 S17449	probable ligand-bi
11	70	15.6	107	2 JC1127	ABC transporter at
12	69	15.3	1633	2 T01369	major allergen cha
13	66.5	14.8	578	2 T24735	hypothetical prote
14	66.5	14.8	3079	1 RGR12	probable gtpase-ac
15	66	14.7	102	2 G97516	hypothetical prote
16	64	14.2	25	2 S26651	uteroglobin precu
17	64	14.2	797	2 D86459	probable disease r
18	63	14.0	92	2 JC1136	major allergen cha
19	62.5	13.9	371	2 E88986	protein C50H11.13
20	62.5	13.9	929	2 C90531	cation-transportin
21	62	13.8	109	2 C56413	major allergen Fel
22	62	13.8	284	2 T36313	probable oxidoredu
23	61.5	13.7	200	2 E72066	riboflavin synthas
24	61.5	13.7	200	2 H86556	hypothetical prote
25	61.5	13.7	416	2 AF2070	RNA-directed DNA p
26	61.5	13.7	1094	2 T00814	Smoc-like regulato
27	61	13.6	340	2 T46942	protein F3P19.18
28	61	13.6	812	2 H86265	major allergen Fel
29	60.5	13.4	92	2 A56413	

30	60.5	13.4	234	2 T31886	hypothetical prote
31	60.5	13.4	315	2 T39444	hypothetical prote
32	60.5	13.4	392	2 A88125	protein T12C9.4 [1
33	60.5	13.4	1390	1 TVH0ME	hepatocyte growth
34	60	13.3	100	2 T11037	hypothetical prote
35	60	13.3	123	2 I51604	cholecystokinin pr
36	60	13.3	246	2 T28166	hypothetical prote
37	60	13.3	346	2 T38750	hypothetical prote
38	60	13.3	664	2 C84869	probable receptor
39	59.5	13.2	244	2 AB1120	conserved hypothet
40	59.5	13.2	247	2 AB1180	conserved hypothet
41	59	13.1	261	2 T43579	type III secretion
42	58.5	13.0	961	2 AE2270	exonuclease ABC C
43	58.5	13.0	1097	2 S68685	adenylate cyclase
44	58	12.9	140	2 H64411	hypothetical prote
45	58	12.9	199	2 C75213	hypothetical prote

ALIGNMENTS

RESULT 1

BOR1

prostatic steroid-binding protein chain C1 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Oct-1982 #sequence-revision 15-Oct-1982 #text-change 22-Jun-1999

C:Accession: A93286; A92348; A90348; S42615; A03252

R:Parker, M.; Needham, M.; White, R.

Nature 298, 92-94, 1982

A:Title: Prostatic steroid binding protein: gene duplication and steroid binding.

A:Reference number: A93286; MUID:82220075; PMID:6896362

A:Accession: A93286

A:Molecule type: mRNA

A:Residues: 1-111 <PAR>

R:Liao, S.; Chen, C.; Huang, I.Y.

J. Biol. Chem. 257, 122-125, 1982

A:Title: Prostate alpha-protein. Complete amino acid sequence of the component that

A:Reference number: A92348; MUID:82055875; PMID:7198120

A:Accession: A92348

A:Molecule type: protein

A:Residues: 24-73,'D','75-89,'E','91,'G','93-111 <LIA>

R:DeLay, B.; Rombaux, W.; Volckaert, G.; Peeters, B.; Mous, J.; Heyns, W.

Biochem. Soc. Trans. 10, 51, 1982

A:Title: Identification of a complementary-DNA clone containing part of the sequence

A:Reference number: A90348

A:Accession: A90348

A:Molecule type: mRNA

A:Residues: 13-14,'S','16,'GG','19-65

R:DeLay, B.; Dirckx, L.; Peeters, B.; Volckaert, G.; Mous, J.; Heyns, W.; Rombaux,

Eur. J. Biochem. 133, 645-649, 1983

A:Title: The nucleotide sequence of cDNA complementary to the C(1) component of rat f

A:Reference number: S42615; MUID:83234456; PMID:6688048

A:Accession: S42615

A:Molecule type: mRNA

A:Residues: 1-3,'IK','6-89,'E','91,'G','93-111 <DEZ>

C:Cross-references: EMBL:V01545; NID:957108; PIDN:CAA24787.1; PID:957109

C:Comment: Steroid-binding protein, the principal secretory protein in rat prostatic

C:Superfamily: uteroglobin

C:Keywords: heterotrimer; prostate; steroid binding

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-111/Product: prostatic steroid-binding protein chain C1 #status experimental <MF>

Query Match 45.8% Score 206; DB 1; Length 111;
Best Local Similarity 49.5%; Pred. No. 1,4e-16;

Matches 45; Conservative 14; Mismatches 30; Indels 2; Gaps 2;

QY 1 MKLSVCLLVTLALCCYQANA-EFCPALVSELDLFFPSLEFLSLAKDPAPPAVAAR 59

DB 4 VELSCLLIM-LAVCCTEANASQICELVAHETT:SLFKSEBELKELEMTNAPPAVAAR 62

QY 60 LGVRCPTDMSLQKRSLIAEVLVKKCSV :0

||||| ||||| | :||| || | || |

A:Residues: 1-96 <SNR>
A:Cross-references: GB:L24372; NID:9461147; PIDN:AA655446.1; PID:9785054
R:Singh, G.; Kalyal, S.L.; Brown, W.E.; Kennedy, A.L.
Exp. Lung Res. 19, 67-75, 1993
A:Title: Mouse Clara cell 10-Kda (CC10) protein: cDNA nucleotide sequence and molecular
A:Reference number: A56656; MUID:93178380; PMID:8440203
A:Accession: A56656
A:Molecule type: mRNA
A:Residues: 1-96 <SIN>
A:Cross-references: EMBL:X67702; NID:949690; PIDN:CAA47936.1; PID:949691
A:Experimental source: lung
A:Note: sequence extracted from NCBI backbone (NCBI:P126148)
A:Note: parts of this sequence, including the amino end of the mature protein, were conf
R:Margat, L.R.; Finegold, M.J.; Stanley, L.A.; Major, A.; Watkins, H.K.; Demayo, F.J.
Am. J. Respir. Cell Mol. Biol. 9, 231-238, 1993
A:Title: Cloning and tissue-specific expression of the cDNA for the mouse Clara cell 10K
A:Reference number: 151925; MUID:94000840; PMID:8398159
A:Accession: 151925
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-96 <RES>
A:Cross-references: GB:L04503; NID:9202313; PIDN:AAA03625.1; PID:9433093
C:Genetics:
A:Introns: 19/1: 81/3
C:Complex: homodimer linked by two disulfide bonds
C:Superfamily: uteroglobin
C:Keywords: lung; steroid binding; uterus
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-96/Product: uteroglobin #status predicted <MAT>
F:24/Disulfide bonds: interchain (to 90) #status predicted
F:90/Disulfide bonds: interchain (to 24) #status predicted
Query Match 22.4%; Score 101; DB 1; Length 96;
Best Local Similarity 28.2%; Pred. No. 0.00018;
Matches 24; Conservative 19; Mismatches 42; Indels 0; Gaps 0;
OY 1 MKLSVCLLVLTALCCYQNAECPALVSELDFFFISEPLFKLSIAKFDAPPEAVAAKL 60
DB 1 MKIAITITVLMISICSSASDDICPGFQVLEALLMESESGYVASLKPPNGSDIQAGN 60
OY 61 GVKRCTDMSLRSLIAEVLVKIL 85
DB 61 QLKRLVDITLPQETRNIVKLTETIL 85
RESULT 7
A36581
polychlorinated biphenyl-binding protein precursor - rat
N:Alternate names: Clara cell 10K secretory protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 20-Aug-1999
C:Accession: A36581; S10185; S21676
R:Nordlund-Moeller, L.; Andersson, O.; Ahlgren, R.; Schilling, J.; Gyllner, M.; Gustaf
J. Biol. Chem. 265, 12690-12693, 1990
A:Title: Cloning, structure, and expression of a rat binding protein for polychlorinated
A:Reference number: A36581; MUID:90324266; PMID:2115324
A:Accession: A36581
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-96 <NOR>
A:Cross-references: GB:J05536; NID:9206039; PIDN:AAA41817.1; PID:9206040
R:Hagen, G.; Wolf, M.; Kalyal, S.L.; Singh, G.; Beato, M.; Suske, G.
Nucleic Acids Res. 18, 2939-2946, 1990
A:Title: Tissue-specific expression, hormonal regulation and 5'-flanking gene region of
A:Reference number: S10185; MUID:90272398; PMID:3349092
A:Accession: S10185
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-18 <HAG>
A:Cross-references: EMBL:X51318; NID:955536; PIDN:CAA35701.1; PID:955537
R:Umland, T.C.; Swaminathan, S.; Furey, W.; Singh, G.; Pletcher, J.; Sax, M.
J. Mol. Biol. 224, 441-448, 1992
A:Title: Refined structure of rat Clara cell 17 kDa protein at 3.0 Å resolution.

A:Reference number: S21676; MUID:92219263; PMID:1560460
A:Contents: annotation, X-ray crystallography, 3.0 angstroms
C:Superfamily: uteroglobin
F:24/Disulfide bonds: interchain (to 90) #status experimental
F:90/Disulfide bonds: interchain (to 24) #status experimental
Query Match 22.2%; Score 100; DB 2; Length 96;
Best Local Similarity 25.9%; Pred. No. 0.00023;
Matches 22; Conservative 22; Mismatches 41; Indels 0; Gaps 0;
OY 1 MKLSVCLLVLTALCCYQNAECPALVSELDFFFISEPLFKLSIAKFDAPPEAVAAKL 60
DB 1 MKIAITITVLMISICSSASDDICPGFQVLEALLMESESGYVASLKPPNGSDIQAGN 60
OY 61 GVKRCTDMSLRSLIAEVLVKIL 85
DB 61 QLKRLVDITLPQETRNIVKLTETIL 85
RESULT 8
UGRBL
uteroglobin precursor - brown hare
N:Alternate names: blastokinin
C:Species: Lepus capensis (brown hare)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
C:Accession: A23825
R:Lopez de Haro, M.S.; Nieto, A.
Biochem. J. 235, 895-898, 1986
A:Title: Nucleotide and derived amino acid sequences of a cDNA coding for pre-uterogl
A:Reference number: A23825; MUID:86323069; PMID:3019311
A:Accession: A23825
A:Molecule type: mRNA
A:Residues: 1-91 <LOP>
A:Cross-references: GB:M25609; NID:9164246; PIDN:AAA30960.1; PID:9164247
A:Experimental source: lung
C:Comment: uteroglobin, synthesized in the uterus and lung, is secreted by the uterus
C:Complex: homodimer linked by two disulfide bonds
C:Superfamily: uteroglobin
C:Keywords: lung; steroid binding; uterus
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-91/Product: uteroglobin #status predicted <MAT>
F:24/Disulfide bonds: interchain (to 90) #status predicted
F:90/Disulfide bonds: interchain (to 24) #status predicted
Query Match 21.6%; Score 97; DB 1; Length 91;
Best Local Similarity 30.2%; Pred. No. 0.00048;
Matches 26; Conservative 15; Mismatches 45; Indels 0; Gaps 0;
OY 1 MKLSVCLLVLTALCCYQNAECPALVSELDFFFISEPLFKLSIAKFDAPPEAVAAKL 60
DB 1 MKITITLVLTALCCSPASAGICPGFAHVIENTLLGTSSYGTSLKFPQDDAMKDAQM 60
OY 61 GVKRCTDMSLRSLIAEVLVKIL 86
DB 61 QMKRVLDITLPQETRNIVKLTETIK 86
RESULT 9
JC2026
cell specific 10K protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: JC2026
R:Ray, M.K.; Magdalen, S.; O'Malley, B.W.; Demayo, F.J.
Biochem. Biophys. Res. Commun. 197, 163-171, 1993
A:Title: Cloning and characterization of the mouse Clara cell specific 10 kDa protein
A:Reference number: JC2026; MUID:94071937; PMID:791613
A:Accession: JC2026
A:Molecule type: DNA
A:Residues: 1-113 <RAY>
C:Comment: This protein is the major secretory product of the Clara cell and binds to
C:Superfamily: uteroglobin
F:73/Region: ochre stop codon

C:Superfamily: Caenorhabditis elegans hypothetical protein T26h2.7

Query Match 14.8%; Score 66.5; DB 2; Length 578;

Best Local Similarity 27.1%; Pred. No. 10;

Matches 23; Conservative 15; Mismatches 38; Indels 9; Gaps 3;

OY 7 LLLVTLALC---CYQANMEFCPALVSELDFFETSEPLFKLSLAKFDAPPEAVAAKLG 62

DB 386 LRVVTVSACEPLAAVPEKPE-CQKELKEFVDFLEASQPDVAFILTRF----FATGVVANS 440

OY 63 KRCTDQMSLOKRSLIAELVTKIKK 87

DB 441 TSSTDILVLEMRQMSKLLPNIKK 465

RESULT 14

RGBY12

probable GTPase-activating protein IRA2 - yeast (Saccharomyces cerevisiae)

M:Alternate names: GLC4 protein; protein O0985; protein YOL081w; protein YOL0951

C:Species: Saccharomyces cerevisiae

C:Date: 30-Sep-1991 #sequence-revision 16-Aug-1996 #text-change 03-Dec-1999

C:Accession: S66775; S66774; A35656; S48254; S50426; S11190; S38505

R:Zumsteln, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.

Submitted to the Protein Sequence Database, July 1996

A:Reference number: S66775

A:Accession: S66775

A:Molecule type: DNA

A:Residues: 1-2423 <ZUM>

A:Cross-references: EMBL:Z74823; GSPDB:GN00015; MIPS:YOL081w

A:Experimental source: strain S288C

R:Alexandarakis, D.; Katsoulou, C.; Tzermela, M.

Submitted to the Protein Sequence Database, July 1996

A:Reference number: S66774

A:Accession: S66774

A:Molecule type: DNA

A:Residues: 1983-3079 <ALE>

A:Cross-references: EMBL:Z74823; GSPDB:GN00015; MIPS:YOL081w

A:Experimental source: strain S288C

R:Tanaka, K.; Nakafuku, M.; Tamanoi, F.; Kaziro, Y.; Matsunoto, K.; Toh-e, A.

Mol. Cell. Biol. 10, 4303-4313, 1990

A:Title: IRA2, a second gene of Saccharomyces cerevisiae that encodes a protein with a G

A:Reference number: A35656; MUID:90318397; PMID:2164637

A:Accession: A35656

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-2308, 'V', 2310-2316, 'I', 2318-3079 <TAN>

A:Cross-references: EMBL:M33779; NID:q171761; PIDN:AAA34710.1; PID:q171762

R:Zumsteln, E.; Griffin, H.; Schweizer, M.

Yeast 10, 1383-1387, 1994

A:Title: Sequence of a 10.27 kb segment on the left arm of chromosome XV from Saccharomy

A:Reference number: S48253; MUID:95208358; PMID:7900427

A:Accession: S48254

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-2423 <ZUM>

A:Cross-references: EMBL:X83121; NID:q600461; PIDN:CAA58201.1; PID:q600480

C:Genetics:

A:Gene: SGD:IRA2; MIPS:YOL081w

A:Cross-references: SGD:S0005441; MIPS:YOL081w

A:Map position: 15L

C:Superfamily: regulatory protein IRA2; ras-specific GAP catalytic domain homology

C:Keywords: transmembrane protein

F:693-709/Domain: transmembrane #status predicted <TM1>

F:1135-1151/Domain: transmembrane #status predicted <TM2>

F:1701-1910/Domain: ras-specific GAP catalytic domain homology <GAP>

F:1842-1858/Domain: transmembrane #status predicted <TM3>

F:2318-2334/Domain: transmembrane #status predicted <TM4>

F:2562-2578/Domain: transmembrane #status predicted <TM5>

Query Match 14.8%; Score 66.5; DB 1; Length 3079;

Best Local Similarity 32.3%; Pred. No. 51;

Matches 20; Conservative 9; Mismatches 18; Indels 15; Gaps 2;

OY 23 FCPALVS---ELDDFFETSEPLFKLSLAK-----FDAPPEAVAAKLGRCND 67

DB 1854 FCPALVSPSENITIDISHSEKRTFSLAKVIONINGSENFSRWPALCSQKDFLECSQ 1913

OY 68 QM 69

DB 1914 RI 1915

RESULT 15

G97516

hypothetical protein AGR_C_2384 [imported] - Agrobacterium tumefaciens (strain C58, C

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence-revision 30-Sep-2001 #text-change 11-Jan-2002

C:Accession: G97516

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: G97516

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-102 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK67088.1; PID:q15156348; GSPDB:GN00169

C:Genetics:

A:Gene: AGR_C_2384

A:Map position: circular chromosome

Query Match 14.7%; Score 66; DB 2; Length 102;

Best Local Similarity 41.2%; Pred. No. 2.1;

Matches 21; Conservative 2; Mismatches 24; Indels 4; Gaps 1;

OY 12 LALCCQAN---AERCPLVSELDFFETSEPLFKLSLAKFDAPPEAVAA 58

DB 37 LALSGLQANMLROAVNDPGLTDFLMSHEPDLMAFCATDTPETVAA 87

Search completed: January 2, 2003, 14:56:02
Job time : 19 secs